





[illegible]

3661	DB	GAATTGCTTGAAACCTGAGCGCGCAGAGGTTGCAGTGTAGGCCAAGATCACGCCACTGCACCTCC	3720
3977	QY	AGCCTGGGTGACAGACGACCTTGTCTTGGAAAAAARAAAAAAGATTTTTTTTTTGT	4036
3721	DB	AGCCTGGGTGACAGCAGACCTTGTCTTGGAAAAAARAAAAAAGATTTTTTTTTTGT	3780
4037	QY	TTGTTGTTTGTGTTGATTTTTGGGGTATTTTTTAGATGGAGTTTTCATCTGTCACTCCAGGC	4096
3781	DB	TTGTTGTTTGTGTTGATTTTTGGGGTATTTTTTAGATGGAGTTTTCATCTGTCACTCCAGGC	3840
4097	QY	TGGAGTGCACCTGGTGCAATCTTGTTGTCATCTGCAACCTCTACCTCCAGGTTCAAGCGAT	4156
3841	DB	TGGAGTGCACCTGGTGCAATCTTGTTGTCATCTGCAACCTCTACCTCCAGGTTCAAGCGAT	3900
4157	QY	CTCATGCTCAGGCTCCCGAGTAGCTGGGACATAGAACAGGCATGAGCCACCATGGCCGC	4216
3901	DB	CTCATGCTCAGGCTCCCGAGTAGCTGGGACATAGAACAGGCATGAGCCACCATGGCCGC	3960
4217	QY	TAATTTTTATATTTTTTAGTAGACAGGGTTTCATCATGCTGGGCAAGCTGGTCTGCTCCT	4276
3961	DB	TAATTTTTATATTTTTTAGTAGACAGGGTTTCATCATGCTGGGCAAGCTGGTCTGCTCCT	4020
4277	QY	GACCTCAGCTGATCCACCCACTCGGCCCTCCAAAGTGTCTGGATTAACAGGCGTAGGCCA	4336
4021	DB	GACCTCAGCTGATCCACCCACTCGGCCCTCCAAAGTGTCTGGATTAACAGGCGTAGGCCA	4080
4337	QY	CCGACCCAGCCGATTTTTGGGGTTTTTTGAGACAGGGTCCCACTCTGTCACTAGACTG	4396
4081	DB	CCGACCCAGCCGATTTTTGGGGTTTTTTGAGACAGGGTCCCACTCTGTCACTAGACTG	4140
4397	QY	GAGTACAGTGATGGGATCATAGCTCACTCAGCCCTTGAATTTCTCCAGGCTCAAGTGCTCC	4456
4141	DB	GAGTACAGTGATGGGATCATAGCTCACTCAGCCCTTGAATTTCTCCAGGCTCAAGTGCTCC	4200
4457	QY	TCCTGCCCGAGCTTCTCAAGTAGCTGGGACTATAGGCCAAGGCCACAACCTAGCTAAT	4516
4201	DB	TCCTGCCCGAGCTTCTCAAGTAGCTGGGACTATAGGCCAAGGCCACAACCTAGCTAAT	4260
4517	QY	TAAAAAAAATGTTTTGTPAGAGATGGAGTCTCACTCATATATTGGCCAGGCTGGTCTT	4576
4261	DB	TAAAAAAAATGTTTTGTPAGAGATGGAGTCTCACTCATATATTGGCCAGGCTGGTCTT	4320
4577	QY	CAACTCCTGGTCTCACTCGATTCTCCTGCCTCAGCCTCCCAAAATGATGGGATACAGGC	4636
4321	DB	CAACTCCTGGTCTCACTCGATTCTCCTGCCTCAGCCTCCCAAAATGATGGGATACAGGC	4380
4637	QY	GTGAGCCATGCACCTGGCCTCAAGTATTTTGTATACAGTATAGGTTGGATCCACAAC	4696
4381	DB	GTGAGCCATGCACCTGGCCTCAAGTATTTTGTATACAGTATAGGTTGGATCCACAAC	4440
4697	QY	AGCTATTTGGTTATTTTTCCGTGCTATCTGGTTTGAATCCAGCTCCACCATTTTTG	4756
4441	DB	AGCTATTTGGTTATTTTTCCGTGCTATCTGGTTTGAATCCAGCTCCACCATTTTTG	4500
4757	QY	GTTCGTGCACATTTCTCAGTTTAAATTAACCTCTCTGCACATTGTTGAATTCCTGTTGTA	4816
4501	DB	GTTCGTGCACATTTCTCAGTTTAAATTAACCTCTCTGCACATTGTTGAATTCCTGTTGTA	4560
4817	QY	AAGTGGAGATGATTAATATGCTCACTATGGAATGTTTTGAAAGATTTAGTAGTCAGACAT	4876
4561	DB	AAGTGGAGATGATTAATATGCTCACTATGGAATGTTTTGAAAGATTTAGTAGTCAGACAT	4620
4877	QY	TTGGGATGGTTCTGCACATATAGCAAGGCCAAAATATATTTTTTTATTTCTTGTAAAT	4936
4621	DB	TTGGGATGGTTCTGCACATATAGCAAGGCCAAAATATATTTTTTTATTTCTTGTAAAT	4680
4937	QY	TATTAATATGACCAATGAGGAAAACGAGTGAATAGTGAGAGGAGATCTTTCCTCTGCATC	4996
4681	DB	TATTAATATGACCAATGAGGAAAACGAGTGAATAGTGAGAGGAGATCTTTCCTCTGCATC	4740
4997	QY	ACTCGGGGTTTTTTTGTGTTTTTTTTTTTTGCTGTGTGACAGGGTCTCACTCTGTTG	5056
4741	DB	ACTCGGGGTTTTTTTGTGTTTTTTTTTTTTGCTGTGTGACAGGGTCTCACTCTGTTG	4800





b	6961	 ATTTCAATCCCCAACTTCTGGTGTCCTCCGCTCATTTTTTCTCCAGAGCACC
y	7277	CATTACCAACCATCAAATAATATGTATTTTAATTTATTTACCATGTTTACAATTTCTGTATCCCT
b	7021	CATTACCAACCATCAAATAATATGTATTTAATTTATTTAACCATGTTTACAATTTCTGTATCCCT
y	7337	CCATTAGGAGTAAACTCCAATGTCACAAAGAGGTTTTTTTTTTTCAITTTGTTTAATGCTG
b	7081	CCATTAGGAGTAAACTCCAATGTCACAAAGAGGTTTTTTTTTTTCAITTTGTTTAATGCTG
y	7397	GGTCCCCACACCAAGAACAGTCCCTGGCACACAGCAGGTGCTCAATGATTATTTGGTACAT
b	7141	GGTCCCCACACCAAGAACAGTCCCTGGCACACAGCAGGTGCTCAATGATTATTTGGTACAT
y	7457	AGAGTGAAGAAGATGGAGCCTCAGGCTGACCTTAGAGAGCAAGGCAGGAGGAAAAGATAAA
b	7201	AGAGTGAAGAAGATGGAGCCTCAGGCTGACCTTAGAGAGCAAGGCAGGAGGAAAAGATAAA
y	7517	AGGGCCCCTCCCTCGGGGTTTTAGAACCTTCCCAACGCCCCCTTAAGCCAGTCTTCTCTGC
b	7261	AGGGCCCCTCCCTCGGGGTTTTAGAACCTTCCCAACGCCCCCTTAAGCCAGTCTTCTCTGC
y	7577	CCCCAGAACCCCGGAACAAACAACAAGTTTCGGCTTCGATAGCTACAGCAGCCCACTTTC
b	7321	CCCCAGAACCCCGGAACAAACAACAAGTTTCGGCTTCGATAGCTACAGCAGCCCACTTTC
y	7637	TGCGACCACTGTGGCTCCCTCTACTACGGGCTTGTGCACACAGGGCATGAAATGCTCCTGT
b	7381	TGCGACCACTGTGGCTCCCTCTACTACGGGCTTGTGTGACCAAGGCGATGAAATGCTCCTGT
y	7697	GAGTGACCTGGGCTTTGCAGGGCCCTTCAAAGCCCGGCTTGGGTTCCGGGAAATGC
b	7441	GAGTGACCTGGGCTTTGCAGGGCCCTTCAAAGCCCGGCTTGGGTTCCGGGAAATGC
y	7757	CCGGAGTGGGGTGGGGGTGGAGTCTTGGCTTTGGGGCGGGGCTCAGTGCTACCCGCA
b	7501	CCGGAGTGGGGTGGGGGTGGAGTCTTGGCTTTGGGGCGGGGCTCAGTGCTACCCGCA
y	7817	GCTTTTCCCTCCAGGCTGGAGATGAACGTGCACCCGGCGCTGTGTGCTGAGGTGCGCTC
b	7561	GCTTTTCCCTCCAGGCTGGAGATGAACGTGCACCCGGCGCTGTGTGCTGAGGTGCGCTC
y	7877	CCTGTGCGGTGGACCAACCCAGCGCCCGGGCGCTCAGCTGAGATCGGGGCTCC
b	7621	CCTGTGCGGTGGACCAACCCAGCGCCCGGGCGCTCAGCTGAGATCGGGGCTCC
y	7937	CACACAGATGAGATCCAGTTAACTGGTGAAGGCCCGCCCTTGGCTGGCCCGGCCCC
b	7681	CACACAGATGAGATCCAGTTAACTGGTGAAGGCCCGCCCTTGGCTGGCCCGGCCCC
y	7997	TCCCCAAAGTGTAGCGGGGCTGACCCCAAGGCACATGTGCTGGCCCGAGCCCTACCCCAA
b	7741	TCCCCAAAGTGTAGCGGGGCTGACCCCAAGGCACATGTGCTGGCCCGAGCCCTACCCCAA
y	8057	GATGGGGCCACGCTCTTTTCTATGGTCAAGCCCACTCCTGACCCCAACCCAAAGGCG
b	7801	GATGGGGCCACGCTCTTTTCTATGGTCAAGCCCACTCCTGACCCCAACCCCAAGGCG
y	8117	AGCACACCCAGCCATACCCCTTTTGGCTCGAAGCCCGGCTCCAACTGGCTTTCTGCAA
b	7861	AGCACACCCAGCCATACCCCTTTTGGCTCGAAGCCCGGCTCCAACTGGCTTTCTGCAA
y	8177	CTTTCTGACCTGTTAAATGACATTTCTTTTCTTTTGGGACGGAGTTTGGCTCT
b	7921	CTTTCTGACCTGTTAAATGACATTTCTTTTCTTTTGGGACGGAGTTTGGCTCT
y	8237	TGTTGCTCAAGCTGGAGTGCAATGGCGGATCTCGGCTCACATGCAACTTTCGCTCCCGG
b	7981	TGTTGCTCAAGCTGGAGTGCAATGGCGGATCTCGGCTCACATGCAACTTTCGCTCCCGG
y	8297	GTTCAAGTGAATTCCTCCTCCCTCAGCCTCCCGAGTAGCTGGGATTAACGGCGGTCTACC

8041	DB	8041	GTTC AAGTGAATCTCTCGCTCGACCTCCGCGAGTAGTGGGATTTACAGGCGCGTGTCCACC	8100
8357	QY	8357	AAGCCCGGCTAAATTTTTTGTATTTTGTAGTACAAACGGGGTTTCAACATGTTAGCCAGGCT	8416
8101	DB	8101	AAGCCCGGCTAAATTTTTTGTATTTTGTAGTACAAACGGGGTTTCAACATGTTAGCCAGGCT	8160
8417	QY	8417	GGTCTCGAACTCTCTGACCCGAGTGATCCCTCTGACTCGCGCTCCCAAAGTGTGGGATT	8476
8161	DB	8161	GGTCTCGAACTCTCTGACCCGAGTGATCCCTCTGACTCGCGCTCCCAAAGTGTGGGATT	8220
8477	QY	8477	AACAGGCGTGAGCCACCGCGCTGGCCAAATGGCTCTCTTTTGTGTTTATTTATTTATGTTTT	8536
8221	DB	8221	AACAGGCGTGAGCCACCGCGCTGGCCAAATGGCTCTCTTTTGTGTTTATTTATTTATGTTTT	8280
8537	QY	8537	ATTTTTTTGAGATGAGGATCTTTGCTCTGTCAACCAGGCTGGAGTGCAGTGGTCAATCTTG	8596
8281	DB	8281	ATTTTTTTGAGATGAGGATCTTTGCTCTGTCAACCAGGCTGGAGTGCAGTGGTCAATCTTG	8340
8597	QY	8597	GCTCACTGCAATCTCTGCCCTCGGGGTTCAAGGGAATTCCTCTGCCCTCAGCCTCCCGAGTA	8656
8341	DB	8341	GCTCACTGCAATCTCTGCCCTCGGGGTTCAAGGGAATTCCTCTGCCCTCAGCCTCCCGAGTA	8400
8657	QY	8657	GCTCGGAATACAGGCGCTGCCACCACTCCGCTAAATTTTTTTTTTTTTTTTTTTTTTTTGA	8716
8401	DB	8401	GCTCGGAATACAGGCGCTGCCACCACTCCGCTAAATTTTTTTTTTTTTTTTTTTTTTTTGA	8460
8717	QY	8717	GACAAGATCTCGCTCTGTGCCCGAGGCTGGAGTGCAGTAGCATGATCTCAGCTCACTGCA	8776
8461	DB	8461	GACAAGATCTCGCTCTGTGTGCCCGAGGCTGGAGTGCAGTAGCATGATCTCAGCTCACTGCA	8520
8777	QY	8777	ACCTCCGCTCTCAGGTTCAAGCGAATTCCTCTGCTTCAGCCTCCTGAGTAGCTGGGACTA	8836
8521	DB	8521	ACCTCCGCTCTCAGGTTCAAGCGAATTCCTCTGCTTCAGCCTCCTGAGTAGCTGGGACTA	8580
8837	QY	8837	CAGGTGCATCAGACTGCACCCAGCTCATTTTTTGTATTTTTTAGTAGAGACGGGTTTCACC	8896
8581	DB	8581	CAGGTGCATCAGACTGCACCCAGCTCATTTTTTGTATTTTTTAGTAGAGACGGGTTTCACC	8640
8897	QY	8897	ATGCTAGCCAGGCTGTGTGGAATCTCTGACCTCAGGTGATCCGCCCGCTCCGCCCTCCC	8956
8641	DB	8641	ATGCTAGCCAGGCTGTGTGGAATCTCTGACCTCAGGTGATCCGCCCGCTCCGCCCTCCC	8700
8957	QY	8957	AAAGTGTCTGGGATTAACAGGGGTGAGACCGTGCCTGGCAATGGCTTTCTGGGTATAAGGA	9016
8701	DB	8701	AAAGTGTCTGGGATTAACAGGGGTGAGACCGTGCCTGGCAATGGCTTTCTGGGTATAAGGA	8760
9017	QY	9017	TCTTTGAGAGGAGAGTACCTGTGTTCTGAGGAGGCTGTGGTTTCAGTACTGTGTGACATGG	9076
8761	DB	8761	TCTTTGAGAGGAGAGTACCTGTGTTCTGAGGAGGCTGTGGTTTCAGTACTGTGTGACATGG	8820
9077	QY	9077	CCAGGTTCCAAACTCTGTGTTCTTAATGAGAGAGAGGCTCTCGATCTGATTTTCAGGTCAC	9136
8821	DB	8821	CCAGGTTCCAAACTCTGTGTTCTTAATGAGAGAGAGGCTCTCGATCTGATTTTCAGGTCAC	8880
9137	QY	9137	CTGGTTTCGGAAGGGCTCTATGCTCTGTCTTCTGGGTTCTGGAGAGGTAAGAAGTCAATG	9196
8881	DB	8881	CTGGTTTCGGAAGGGCTCTATGCTCTGTCTTCTGGGTTCTGGAGAGGTAAGAAGTCAATG	8940
9197	QY	9197	AGAAACGAGACTGAGAGCTTGGAATTCCTTTTTTTTTTTTTTTTTTTTTTTTGAACGAGTCTCGCTG	9256
8941	DB	8941	AGAAACGAGACTGAGAGCTTGGAATTCCTTTTTTTTTTTTTTTTTTTTTTTTGAACGAGTCTCGCTG	9000
9257	QY	9257	TGACGCCCGAGGTGAGTGCAGTGGGTAACTCCGGCTCACTGCAGCTCCGACCTCCTGG	9316
9001	DB	9001	TGACGCCCGAGGTGAGTGCAGTGGGTAACTCCGGCTCACTGCAGCTCCGACCTCCTGG	9060
9317	QY	9317	GTTCAGGTCAATCTCCCGCTCAGCCTCTCTGAGTAGCTGGGACCAACAGACCTGCCACC	9376
9061	DB	9061	GTTCAGGTCAATCTCCCGCTCAGCCTCTCTGAGTAGCTGGGACCAACAGACCTGCCACC	9120
9377	QY	9377	ACGCCCGAGCTAAATTTTTTTTTTTTTTTTTTTTTTTTGTATTTTTTAGTGGAGACGGGTTTCAACATCA	9436
9121	DB	9121	ACGCCCGAGCTAAATTTTTTTTTTTTTTTTTTTTTTTTGTATTTTTTAGTGGAGACGGGTTTCAACATCA	9180

QY	9437	CAGATGGTCTCGATCTCTGACCTTGTGATCCGCGCCCTTGCGCTCCCAAGTGTGG	10517	CTCCGCAACGACTCTCATGGGGCCATGTCTTTGGCGTCTCGAGCTGCTCAAGGGCC	10576
DB	9181	CAGATGGTCTCGATCTCTGACCTTGTGATCCGCGCCCTTGCGCTCCCAAGTGTGG	10261	CTCCGCAACGACTCTCATGGGGCCATGTCTTTGGCGTCTCGAGCTGCTCAAGGGCC	10320
QY	9497	GATTACAGGCATGAGCCCGCTGCTGCGCAAGCTTGGAACCTCTTGATGTGACTGGAG	10577	CGTGGATGGCTGCTGAGGAGCAGGGCTGGGGCTGGGGATGGAGCGCAATATTACCATCT	10636
DB	9241	GATTACAGGCATGAGCCCGCTGCTGCGCAAGCTTGGAACCTCTTGATGTGACTGGAG	10321	CGTGGATGGCTGCTGAGGAGCAGGGCTGGGGCTGGGGATGGAGCGCAATATTACCATCT	10380
QY	9557	GAGGGCTGGGAGCCCTTCTGGAATCTCTAAACCGTCAACCTTCCTCACTCCCGCTTT	10637	CAATCTGTGTGGTCTCTCTCTCCAGGCCACTGTCTTCCCTCTGCTCCCTCCAGCATGC	10696
DB	9301	GAGGGCTGGGAGCCCTTCTGGAATCTCTAAACCGTCAACCTTCCTCACTCCCGCTTT	10381	CAATCTGTGTGGTCTCTCTCTCCAGGCCACTGTCTTCCCTCTGCTCCCTCCAGCATGC	10440
QY	9617	AGTTGGCGAGCCCGTAACTTCTATCGAACCCAAATGGTCTCTCTGATCCCTATGT	10697	GCAC	10756
DB	9361	AGTTGGCGAGCCCGTAACTTCTATCGAACCCAAATGGTCTCTCTGATCCCTATGT	10441	GCAC	10500
QY	9677	GAACCTGAAGCTCATCCAGACCTTCGGAACCTTGACGAACACAGAAAGCCGAA	10757	ATTCTTCTCTTCTTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	10816
DB	9421	GAACCTGAAGCTCATCCAGACCTTCGGAACCTTGACGAACACAGAAAGCCGAA	10501	ATTCTTCTCTTCTTCT	10560
QY	9737	AGCCACGCTAAACCTGTGGAATGAGACCTTTGTGTGTGATCTGCGGTGACGGAA	10817	TCTCTTCCATCTCTGTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	10876
DB	9796	AGCCACGCTAAACCTGTGGAATGAGACCTTTGTGTGTGATCTGCGGTGACGGAA	10561	TCTCTTCCATCTCTGTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	10620
QY	9481	AGCCACGCTAAACCTGTGGAATGAGACCTTTGTGTGTGATCTGCGGTGACGGAA	10877	TCTCTTCCATCTCTGTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	10936
DB	9797	GGCAATGACAGCTGACAGAGATGATCTGAGGGTCTAGTGGCCCCCAGAGAGCAGCTGA	10621	TCTCTTCCATCTCTGTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	10680
QY	9541	GGCAATGACAGCTGACAGAGATGATCTGAGGGTCTAGTGGCCCCCAGAGAGCAGCTGA	10937	AGTTACTGAACACAGAGAGGGCGAGTATTACATGTGCGGTGGCCGATGCTGACAA	10996
DB	9857	TGGGAGGGTTAGGATAGAGGAACCCAGAAAGGGCAGAAAGATGTTGGGAAAGGG	10681	AGTTACTGAACACAGAGAGGGCGAGTATTACATGTGCGGTGGCCGATGCTGACAA	10740
QY	9601	TGGGAGGGTTAGGATAGAGGAACCCAGAAAGGGCAGAAAGATGTTGGGAAAGGG	10997	TGAGGCTCTCTCAGAGTGTGAGGTACCCAGACCTTGGCTTCTCAAGGGAGCCAGCC	11056
DB	9917	AATAGAGTGTAGGAGGTGGGATGAGATACAGAAACGGAGAGACAGCCAGACCACTG	10741	TGAGGCTCTCTCAGAGTGTGAGGTACCCAGACCTTGGCTTCTCAAGGGAGCCAGCC	10800
QY	9661	AATAGAGTGTAGGAGGTGGGATGAGATACAGAAACGGAGAGACAGCCAGACCACTG	11057	CAGGCTCTCTCAGAGTGTGAGGTACCCAGACCTTGGCTTCTCAAGGGAGCCAGCC	11116
DB	9977	TATTAATTAGTCTCAATTGAGCCCTTCTAGAGTTAGACAGATGAGAGAGAGAG	10801	CAGGCTCTCTCAGAGTGTGAGGTACCCAGACCTTGGCTTCTCAAGGGAGCCAGCC	10860
QY	9721	TATTAATTAGTCTCAATTGAGCCCTTCTAGAGTTAGACAGATGAGAGAGAGAG	1117	GACTAGGTTCCAGAGACCTTAGGACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	11176
DB	10037	AGAGAGTCTCAGAGAGCGAGAAACCCAGAGAGACACAGATGGAGAGGGAGAGAA	10861	GACTAGGTTCCAGAGACCTTAGGACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	10920
QY	9781	AGAGAGTCTCAGAGAGCGAGAAACCCAGAGAGACACAGATGGAGAGGGAGAGAA	11177	CCAGGTTCTGATGGGAATTATAGTCTCTATCTATCGCATGCTTGAGGCTAGAGGGC	11236
DB	10097	GATGGGGATGGCAGGAGACAGAGATCAGTTGACAGAGACAGAGTGTATAGAGACCA	10921	CCAGGTTCTGATGGGAATTATAGTCTCTATCTATCGCATGCTTGAGGCTAGAGGGC	10980
QY	9841	GATGGGGATGGCAGGAGACAGAGATCAGTTGACAGAGACAGAGTGTATAGAGACCA	11237	CACAGCCCCCTGTTTAGGGCGATCCCTGCACTCTTTGGGACCCCTGACTCTCTCTTTCT	11296
DB	10157	GAGAGGAGAGAGGGTACAGAGCTCAGAGAGAGATCTCGAGAGACAGACAGAGAG	10981	CACAGCCCCCTGTTTAGGGCGATCCCTGCACTCTTTGGGACCCCTGACTCTCTCTTTCT	11040
QY	9901	GAGAGGAGAGAGGGTACAGAGCTCAGAGAGAGATCTCGAGAGACAGAGACAGAG	11297	TTTCTCCAGGCTTGTAACCTACCCCTGGAAATGATAGGTGAGGTAGAGTAGACAGGGGCTT	11356
DB	10217	TGGGAAGGGCGGAGATGACAGGAGGAGGAGAGAGCTCTCTAGGTTTACTTCTAG	11041	TTTCTCCAGGCTTGTAACCTACCCCTGGAAATGATAGGTGAGGTAGAGTAGACAGGGGCTT	11100
QY	9961	TGGGAAGGGCGGAGATGACAGGAGGAGGAGAGAGCTCTCTAGGTTTACTTCTAG	11357	GAATGGAGGAGGTTTGGCTACTTCTCTGATTTCTTATTTCTCTCTCTCTCTCTCTCT	11416
DB	10277	GCCCCAAGCCCTTAGCTGGAGAGAGAGCCCGGCTGGGAGGTGAGAGTGGAGACCGAC	11101	GAATGGAGGAGGTTTGGCTACTTCTCTGATTTCTTATTTCTCTCTCTCTCTCTCTCT	11160
QY	10021	GCCCCAAGCCCTTAGCTGGAGAGAGAGCCCGGCTGGGAGGTGAGAGTGGAGACCGAC	11417	CAATTTCCCAACACATGAGTTGAGCAACATTTGTGTAGGCTGTCTTGTGCTGTGAA	11476
DB	10337	AAACGAGAGAGAGCCCGCTGCTGGGTTTCCCGCCCTCCAGCACCAGAGGATGGG	11161	CAATTTCCCAACACATGAGTTGAGCAACATTTGTGTAGGCTGTCTTGTGCTGTGAA	11220
QY	10081	AAACGAGAGAGAGCCCGCTGCTGGGTTTCCCGCCCTCCAGCACCAGAGGATGGG	11477	TAAATCAGGATCCAGAGTGAATCTGACCCCTCAAGCAACTCTCAAGGTAGGAGACAGT	11536
DB	10397	GAACCGAGGGAGCCAGCTCGGCTCTGACCCCATCCACCCCATCTTCTCTGAGCAA	11221	TAAATCAGGATCCAGAGTGAATCTGACCCCTCAAGCAACTCTCAAGGTAGGAGACAGT	11280
QY	10141	GAAACGAGGGAGCCAGCTCGGCTCTGACCCCATCCACCCCATCTTCTCTGAGCAA	11537	CACAGATCTTAAATACAGAAAGATGTCTAAATTAGAGGTAGCCAGGGCCTCTGAAGA	11596
DB	10457	CCTGAAGCCAGGGATGTGAGAGCCCGGCTCAGCGTGGAGGTGTGGAGCTGGGACCGGAC	11281	CACAGATCTTAAATACAGAAAGATGTCTAAATTAGAGGTAGCCAGGGCCTCTGAAGA	11340
QY	10201	CCTGAAGCCAGGGATGTGAGAGCCCGGCTCAGCGTGGAGGTGTGGAGCTGGGACCGGAC	11597	GGCCTTAACGAGGACCTAATTCACGCTGGGGGAGGGTGTGAGGGAGGACTTCTCCCTGAGG	11656

11341	GGCCTTAACGAGGCACTAATCCAGCTCGGGAGGCTGGTCAGGAGGACTTCCCTGAGG	11400	12421	TTAGAGCGTGAGCGACCAACGCCAGAGCAATACCCATTTTCTAGGCTGTATAGCCAG	12480
11657	AGGTGACGCTGAATGATCTTGAGGTTTAAATTTTAAATTTTAAATTTTAAATTTT	11716	12737	GCCTGTCTCGGGAATAGAAATCAGGCCATTTCCCTGGTGGAGCTCTTCTTAGTGGAGA	12796
11401	AGGTGACGCTGAATGATCTTGAGGTTTAAATTTTAAATTTTAAATTTTAAATTTT	11460	12481	GCCTGTCTCGGGAATAGAAATCAGGCCATTTCCCTGGTGGAGCTCTTCTTAGTGGAGA	12540
11717	ATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT	11776	12797	CAAAAGTTACAAAACCCAGACATTTCAACGAGGAGCAATGCTGCTGTAAATGAGACAGCT	12856
11461	ATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT	11520	12541	CAAAAGTTACAAAACCCAGACATTTCAACGAGGAGCAATGCTGCTGTAAATGAGACAGCT	12600
11777	CAACCTCCAGCTCCCGGTTCAAGCAATTTCTCTGCTCAGGCTCCTGAGTAGCTGGAT	11836	12857	CAGGCACTGGGGCTCCCTGGGCA CAGGCTGAGTCAGAGAAAAGCTTCTTAGAGAGTGAGA	12916
11521	CAACCTCCAGCTCCCGGTTCAAGCAATTTCTCTGCTCAGGCTCCTGAGTAGCTGGAT	11580	12601	CAGGCACTGGGGCTCCCTGGGCA CAGGCTGAGTCAGAGAAAAGCTTCTTAGAGAGTGAGA	12660
11837	TACAGGTGACCGCCACCA CACCCAGCTAATTTTAAATTTTAAATTTTAAATTTT	11896	12917	CCTGTAAGAGGGCGGGATTTCCCAAGGAGAGAC CAGATTTTTCAGGCGAGGAGGAATAA	12976
11581	TACAGGTGACCGCCACCA CACCCAGCTAATTTTAAATTTTAAATTTTAAATTTT	11640	12661	CCTGTAAGAGGGCGGGATTTCCCAAGGAGAGAC CAGATTTTTCAGGCGAGGAGGAATAA	12720
11897	TGCCCATGTTGGCCAGGCTGATCTCAAACTCCCAAACTCAGGTGATCCGCTTGGC	11956	12977	TGCTCTCTCCCTCAATTTTACCCCTTTCAAAAAATATCTTTACAGAGCATCTTTGTGTCAGG	13036
11641	TGCCCATGTTGGCCAGGCTGATCTCAAACTCCCAAACTCAGGTGATCCGCTTGGC	11700	12721	TGCTCTCTCCCTCAATTTTACCCCTTTCAAAAAATATCTTTACAGAGCATCTTTGTGTCAGG	12780
11957	CTCCCAAAGTGTGGGATTAAGGCAATGACCACTGCGCCCAACCGATTTCTGAGTTTTT	12016	13037	CGTGGCTCTACTCTGCGGATATAGAGAAAGAGGAGGAAAGAA CAAACAAACAAACAA	13096
11701	CTCCCAAAGTGTGGGATTAAGGCAATGACCACTGCGCCCAACCGATTTCTGAGTTTTT	11760	12781	CGTGGCTCTACTCTGCGGATATAGAGAAAGAGGAGGAAAGAA CAAACAAACAAACAA	12840
12017	TATTTTATTTTGTAGACGAGTCTCGCTGTAGCGCCAGGCTGGAGTGCAGTGGCAT	12076	13097	AAGTTCTCTTCTTATCGGATTTTACACCGGAGGAGCAATTTAAACAAATATATATAGCA	13156
11761	TATTTTATTTTGTAGACGAGTCTCGCTGTAGCGCCAGGCTGGAGTGCAGTGGCAT	11820	12841	AAGTTCTCTTCTTATCGGATTTTACACCGGAGGAGCAATTTAAACAAATATATATAGCA	12900
12077	CTCGGCTCACTGCAAGCTCCGCTCTCTGGGTTACGCCATTTCTCTGATCAGCCCTCTG	12136	13157	TATGATAGACTGGCAGCATGCTCATGTCTGTGATCTCTAGTAAGGCGGGCGGATCACCT	13216
11821	CTCGGCTCACTGCAAGCTCCGCTCTCTGGGTTACGCCATTTCTCTGATCAGCCCTCTG	11880	12901	TATGATAGACTGGCAGCATGCTCATGTCTGTGATCTCTAGTAAGGCGGGCGGATCACCT	12960
12137	AGTAGCTGGGACTACAGGCGGCCACACCAATCCCGGGCTAAATTTTGTATTTTAGTAG	12196	13217	GAGTCAAGAGTTTGAGAC CAGCCCTGGCCAGCTGGCGAAACCCCATCTCTACTAAAAAA	13276
11881	AGTAGCTGGGACTACAGGCGGCCACACCAATCCCGGGCTAAATTTTGTATTTTAGTAG	11940	12961	GAGTCAAGAGTTTGAGAC CAGCCCTGGCCAGCTGGCGAAACCCCATCTCTACTAAAAAA	13020
12197	AGATGGGTTTACCGTGTAGCAGGATGCTCGATCTCTGACCTGGTGATCCACCC	12256	13277	TACAAAAATCAGCTGGGCTGGTGAGGCGCTGTAATCCAGCTACTCGGAAGGCTGAG	13336
11941	AGATGGGTTTACCGTGTAGCAGGATGCTCGATCTCTGACCTGGTGATCCACCC	12000	13021	TACAAAAATCAGCTGGGCTGGTGAGGCGCTGTAATCCAGCTACTCGGAAGGCTGAG	13080
12257	GCTCAGGCTCCCAAGTGTGGGATTAAGCGGCTGAGCCACACACCCAGCCGATCTT	12316	13337	GCAGGAAATTTGCTGGATTCGGGAAGTAGAGGCTGAGTGAGCCAGATCGCTCCACTG	13396
12001	GCTCAGGCTCCCAAGTGTGGGATTAAGCGGCTGAGCCACACACCCAGCCGATCTT	12060	13081	GCAGGAAATTTGCTGGATTCGGGAAGTAGAGGCTGAGTGAGCCAGATCGCTCCACTG	13140
12317	GAGTTTTAAAAAATCTATCAAGCATGATCATCTTAATCTCTCCATTCATTCACTCA	12376	13397	CACCTCAGCCTGGATGACAGAGGAGACTGTCTCAAAAAA AAAAAA AAAAAA AAAAAA	13456
12061	GAGTTTTAAAAAATCTATCAAGCATGATCATCTTAATCTCTCCATTCATTCACTCA	12120	13141	CACCTCAGCCTGGATGACAGAGGAGACTGTCTCAAAAAA AAAAAA AAAAAA AAAAAA	13200
12377	CTGAATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	12436	13457	GACAAGAAATCTTCAAGATTCAAACACAGCAACACATGTTATAGTCTTTACTGGACTCTT	13516
12121	CTGAATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	12180	13201	GACAAGAAATCTTCAAGATTCAAACACAGCAACACATGTTATAGTCTTTACTGGACTCTT	13260
12437	TTTTGTCAACCAAGTGTGAGTGCAGTGCAGTCTCAGCTCAGCTGCAACCTCTGCTCC	12496	13517	ACAGAAATCTTCAACAGATTTTAAATGTTGTGTGGGGTTCACTGCAATCAGAAATTC	13576
12181	TTTTGTCAACCAAGTGTGAGTGCAGTGCAGTCTCAGCTCAGCTGCAACCTCTGCTCC	12240	13261	ACAGAAATCTTCAACAGATTTTAAATGTTGTGTGGGGTTCACTGCAATCAGAAATTC	13320
12497	CAGATTCAAGTGATTTCTCTGCTCAGGCTCCTGAGTAGTGGGATTAACAGAGCGCAC	12556	13577	CTAGAGTCTTGTCTTTTAAAGCACTTCCCGCCCTTCTGCGAGCTACTCTAGTGACG	13636
12241	CAGATTCAAGTGATTTCTCTGCTCAGGCTCCTGAGTAGTGGGATTAACAGAGCGCAC	12300	13321	CTAGAGTCTTGTCTTTTAAAGCACTTCCCGCCCTTCTGCGAGCTACTCTAGTGACG	13380
12557	ACCACACTGGCTAATTTTGTATTTTGTATGATGATGGGTTTCGACATGTTGGCCAGG	12616	13637	ATCTCTCTGATGCTCAAAATGTTCTGCTACTTAAATTAATTTCTCAGGTGATCTTTTGCA	13696
12301	ACCACACTGGCTAATTTTGTATTTTGTATGATGATGGGTTTCGACATGTTGGCCAGG	12360	13381	ATCTCTCTGATGCTCAAAATGTTCTGCTACTTAAATTAATTTCTCAGGTGATCTTTTGCA	13440
12617	CTGGTCTCGAACTCTGACCTCAAGTGTATCCACCGCTTGGCTCCCAAGCGCTGAGA	12676	13697	AAGTTAAAGTTTGAATGAGGCTCTGCGCCCGGCGCAGTGGCTCACGCCCTGTCTATCCAG	13756
12361	CTGGTCTCGAACTCTGACCTCAAGTGTATCCACCGCTTGGCTCCCAAGCGCTGAGA	12420	13441	AAGTTAAAGTTTGAATGAGGCTCTGCGCCCGGCGCAGTGGCTCACGCCCTGTCTATCCAG	13500
12677	TTAGAGGCGGTGAGCGACCA CCGCCAGAGCAATACCCATTTTCTAGGCTGTCTAAGCCAG	12736	13757	CACTTTGGGAGGCCAAGCGGGTGGATTCACAGGTCAAGGAGATCAGACCACTCTCTGGCTA	13816
			13501	CACTTTGGGAGGCCAAGCGGGTGGATTCACAGGTCAAGGAGATCAGACCACTCTCTGGCTA	13560

13817	ACA	CGGTGAATCCC	CGTCTCTACTAAAAATACAAAAAATTAGCTGGCGCTGGTGGTGGG	13876	
13561	ACA	CGGTGNA	TCCC	CGTCTCTACTAATAATACAAAAAATTAGCTGGCGGTGGTGGG	13620
13877	TGC	TGTAGTCC	CAGGTACTCAGGAGGCTGAGGAGGAAATGGCATGAACTCGGAGGT	13936	
13621	TGC	TGTAGTCC	CAGGTACTCAGGAGGCTGAGGAGGAAATGGCATGAACTCGGAGGT	13680	
13937	GGAG	CTTGCAATGAG	CGGAGATCGGTGCCACTGCACTACAGCTCGGTGACAGAGCGAGAC	13996	
13681	GGAG	CTTGCAATGAG	CGGAGATCGGTGCCACTGCACTACAGCTCGGTGACAGAGCGAGAC	13740	
13997	TCTAT	CTCAGAAAAA	AAAAAAGAGAGAAATGGGCTCTGCAGGAGACAAGGGTACACAGC	14056	
13741	TCTAT	CTCAGAAAAA	AAAAAAGAGAGAAATGGGCTCTGCAGGAGACAAGGGTACACAGC	13800	
14057	GGGAG	GACATCTTGAG	CCAAAGAGGTAGAGTCTTTTGAGATCAGCAGGGATGATCCTCCC	14116	
13801	GGGAG	GACATCTTGAG	CCAAAGAGGTAGAGTCTTTTGAGATCAGCAGGGATGATCCTCCC	13860	
14117	GTA	CAAA	CCCAAGAAACCCAGCAGGCGAGATGGTGGGCAAAAGGCTAGAGCAGGAGTG	14176	
13861	GTA	CAAA	CCCAAGAAACCCAGCAGGCGAGATGGTGGGCAAAAGGCTAGAGCAGGAGTG	13920	
14177	TAGG	TGGTGTGTG	CCCTGTTGTGGCTCACAGCACTCTCCCA	CAGTTTCAGCAGGCCACA	14236
13921	TAGG	TGGTGTGTG	CCCTGTTGTGGCTCACAGCACTCTCCCA	CAGTTTCAGCAGGCCACA	13980
14237	CTTA	TATATCAAT	GAACA	CCAACTCTGTGCCAAGCCTTGAGCTAGGTAGTACGGGGCTAAC	14296
13981	CTTA	TATATCAAT	GAACA	CCAACTCTGTGCCAAGCCTTGAGCTAGGTAGTACGGGGCTAAC	14040
14297	AAC	CAGCAAA	CAGAAACAGCCCTGATTATTATTATTATTATTATTATTATTATTAT	14356	
14041	AAC	CAGCAAA	CAGAAACAGCCCTGATTATTATTATTATTATTATTATTATTATTAT	14100	
14357	TATT	TATTATTAT	TATATCTATTTTGAGACACAGTCTCGCTCTGTCTGCCCAGGCTGGAA	14416	
14101	TATT	TATTATTAT	TATATCTATTTTGAGACACAGTCTCGCTCTGTCTGCCCAGGCTGGAA	14160	
14417	TGC	AGTGAGCGAT	CTCAGCTCAGCTGCAACCTCTGCCCTCCCGGGTTCAAGCGATTCTCCT	14476	
14161	TGC	AGTGAGCGAT	CTCAGCTCAGCTGCAACCTCTGCCCTCCCGGGTTCAAGCGATTCTCCT	14220	
14477	GCCT	TGGGCTCC	CAAGTAGTGGGACTACAGGCATGTGCCACCATGTCTACTAATTTTT	14536	
14221	GCCT	TGGGCTCC	CAAGTAGTGGGACTACAGGCATGTGCCACCATGTCTACTAATTTTT	14280	
14537	ATATT	GCTAGTAGAT	GGGCTTCGCCATGTTGGCAGGCTGGTCTTTGAATCCTCGACC	14596	
14281	ATATT	GCTAGTAGAT	GGGCTTCGCCATGTTGGCAGGCTGGTCTTTGAATCCTCGACC	14340	
14597	TCAG	TGTATTCGCC	CACCTCGGCCCTCCAAAGTGTGGGATTTACAGGCATGAGCCACCGC	14656	
14341	TCAG	TGTATTCGCC	CACCTCGGCCCTCCAAAGTGTGGGATTTACAGGCATGAGCCACCGC	14400	
14657	ACCC	AGCCCTCA	ACAAATATTATGTAGCTCAATGAGGTAGGCAAGTGTACTGTGTCTT	14716	
14401	ACCC	AGCCCTCA	ACAAATATTATGTAGCTCAATGAGGTAGGCAAGTGTACTGTGTCTT	14460	
14717	AGCG	AAACAA	AGCAGACCCCTGCTTTAGGGAGCTCACAGCAGAAAGCAGATGATCACACA	14776	
14461	AGCG	AAACAA	AGCAGACCCCTGCTTTAGGGAGCTCACAGCAGAAAGCAGATGATCACACA	14520	
14777	GAT	AGATGTAAAT	TACTAAGAAATAAAAGTGCAGGAAGGTGTCTTCATGTGTGACCAAGG	14836	
14521	GAT	AGATGTAAAT	TACTAAGATATAAGTGCAGGAAGGTGTCTTCATGTGTGACCAAGG	14580	
14837	GGT	GTAAGAGG	CATCTGACCCAGTTTTAAAGATCAGGCGAGGCCTCTATGAAGTAT	14896	
14581	GGT	GTAAGAGG	CATCTGACCCAGTTTTAAAGATCAGGCGAGGCCTCTATGAAGTAT	14640	

Qy	14897	GCTTGAGTCAAGGTCTAAAGGGTGTTTGGGAGACAACCTAGAGGAGAAAGGGAGGGGAGAG	14955
Db	14641	GCTTGAGTCAAGGTCTAAAGGGTGTTTGGGAGACAACCTAGAGGAGAAAGGGAGGGGAGAG	14700
Qy	14957	CTTTACAGGAAGACCTACAGGCACATCAGAGGCCCTCAGGTGGGAGGAGGACAATCAG	15016
Db	14701	CTTTACAGGAAGACCTTAACGGCACATCAGAGGCCCTCAGGTGGGAGGAGGACAATCAG	14760
Qy	15017	TGTCAGGCCCAGGGTGGCTGGACCATGAGCCCTGGGAGAGAGAACAACCTGCAGTGTC	15076
Db	14761	TGTCAGGCCCAGGGTGGCTGGACCATGAGCCCTGGGAGAGAGAACAACAACCTGCAGTGTC	14820
Qy	15077	AGTCTCAGCCTGGCTCTCGAAGTCATGTGGAAATAAATCTTAAACACAGAGGAGCAGTTA	15136
Db	14821	AGTCTCAGCCTGGCTCTCGAAGTCATGTGGAAATAAATCTTAAACACAGAGGAGCAGTTA	14880
Qy	15137	AAGGGTTTACAAGCATAGGGGAGACATGACCTGGTTATTTATTTTAAATTTGGCTCCCTG	15196
Db	14881	AAGGGTTTACAAGCATAGGGGAGACATGACCTGGTTATTTATTTTAAATTTGGCTCCCTG	14940
Qy	15197	TGCCTGCTCAGTAGAAGATGCAATTAGAAGGGCAGCCGCTCCATGTAGAGGACAAGTGTC	15256
Db	14941	TGCCTGCTCAGTAGAAGATGCAATTAGAAGGGCAGCCGCTCCATGTAGAGGACAAGTGTC	15000
Qy	15257	GAAGCTGTGACAGCAGCTTAGTCTTTGGGCCCTCTCCCTGGGGGGCCGAGGACGAGAAAGG	15316
Db	15001	GAAGCTGTGACAGCAGCTTAGTCTTTGGGCCCTCTCCCTGGGGGGCCGAGGACGAGAAAGG	15060
Qy	15317	TAGAGAAAGGACCTTAGCTGAAGCCAGGTGTGCTCCCTGGACCTGGCAGCACCCATGTCA	15376
Db	15061	TAGAGAAAGGACCTTAGCTGAAGCCAGGTGTGCTCCCTGGACCTGGCAGCACCCATGTCA	15120
Qy	15377	CCCAGAAGCTTTTACACATAACGATCTCAGGTCGCCACCCACAGATTTATAGAGTTAGAA	15436
Db	15121	CCCAGAAAGCTTTTACACATAACGATCTCAGGTCGCCACCCACAGATTTATAGAGTTAGAA	15180
Qy	15437	AATCTGGCAGTGGGACCCAGCAGCAATCTGTTTACAAACCCCTCTAGGAAATTCGGCTTAG	15496
Db	15181	AATCTGGCAGTGGGACCCAGCAGCAATCTGTTTACAAACCCCTCTAGGAAATTCGGCTTAG	15240
Qy	15497	AGGCTAAGAGCAACAGATTCCTAGAGCTGGACTGCTCGGTTTCATTTCTGGCTCTGTCC	15556
Db	15241	AGGCTAAGAGCAACAGATTCCTAGAGCTGGACTGCTCGGTTTCATTTCTGGCTCTGTCC	15300
Qy	15557	TTTACCTGCTGTGACTTTGGGGCAAGTTACTTAAACGTCCTGTGCTAGTCTCCTTTCT	15616
Db	15301	TTTACCTGCTGTGACTTTGGGGCAAGTTACTTAAACGTCCTGTGCTAGTCTCCTTTCT	15360
Qy	15617	GTAAATGAAACGATAGCAGGGTTTTCTGGAAACAGCATATGATAAGCTATCTAAAAAA	15676
Db	15361	GTAAATGAAACGATAGCAGGGTTTTCTGGAAACAGCATATGATAAGCTATCTAAAAAA	15420
Qy	15677	AAAAAGAGRAAAAAAGAGCTAAGTGTGTTGTTGAATAATAATAAACCCCTCCAGGCTAT	15736
Db	15421	AAAAAGAGRAAAAAAGAGCTAAGTGTGTTGTTGAATAATAATAAACCCCTCCAGGCTAT	15480
Qy	15737	GGGAGTCAAGAAAAATTAAAGCCAAAGGACAGGGTAGGAGGTGGCCATTTTCTCTGTCT	15796
Db	15481	GGGAGTCAAGAAAAATTAAAGCCAAAGGACAGGGTAGGAGGTGGCCATTTTCTCTGTCT	15540
Qy	15797	AGCGATTCATCCTTCCTTTCTTTGGGTCTGTGTCTCTTGGGAGCAATTCCTTATCGC	15856
Db	15541	AGCGATTCATCCTTCCTTTCTTTGGGTCTGTGTCTCTTGGGAGCAATTCCTTATCGC	15600
Qy	15857	TGTGTAAGTCTAACTGCTCTGGCTCTTTCTTTCTTTCTTTCCACAGCGGTGCGGATGG	15916
Db	15601	TGTGTAAGTCTAACTGCTCTGGCTCTTTCTTTCTTTCTTTCTTTCCACAGCGGTGCGGATGG	15660
Qy	15917	GCCTCTTTCTCTCCATCCCTCTCCCTTTCCCTTAGTCCCAACGACCCCAAGCGCTGCT	15976
Db	15661	GCCTCTTTCTCTCCATCCCTCTCCCTTTCCCTTAGTCCCAACGACCCCAAGCGCTGCT	15720
Qy	15977	TCTTCGGGGCGAGTCCAGGACGCTGCACATCTCCGATCTTACGTTCTCTCATGGTCTTAG	16036

b 15721 TCTCGGGCGAGTCAGACGCTGCACATCTCCGACTTCAGCTTCCTCATGGTTCTAG 15780  
y 16037 GAAAGGCGAGTTTGGGAAAGTTTGGATTCCTGGGGTTCTGGGGGAAAGGAGGATGTCTG 16096  
b 15781 GAAAGGCGAGTTTGGGAAAGTTTGGATTCCTGGGGTTCTGGGGGAAAGGAGGATGTCTG 15840  
y 16097 TCGGAAGGTCAGATTCTGGTTCTTAGGAGGAGAGTGGGGGTGGGAGAGACTGGGCTCC 16156  
b 15841 TGGGAAGGTCAGATTCTGGTTCTTAGGAGGAGAGTGGGGGTGGGAGAGACTGGGCTCC 15900  
y 16157 TGCATCTTCAAAATATAGTTAGTTGGGCGGTTTCAAGTTCTCTGGAGAGAGGTTTACAG 16216  
b 15901 TGCATCTTCAAAATATAGTTAGTTGGGCGGTTTCAAGTTCTCTGGAGAGAGGTTTACAG 15960  
y 16217 ATGTGCACTCTCTTGGAGGAGCGGGCGCAAGTCAGGGCTGTGATCCTTAAAGAGA 16276  
b 15961 ATGTGCACTCTCTTGGAGGAGCGGGCGCAAGTCAGGGCTGTGATCCTTAAAGAGA 16020  
y 16277 TGGAGGAAGGGCTGGGATCCCGTTTCCCTGCGTCCCTTAGGGAGGGGCGAGGTCCTGTA 16336  
b 16021 TGGAGGAAGGGCTGGGATCCCGTTTCCCTGCGTCCCTTAGGGAGGGGCGAGGTCCTGTA 16080  
y 16337 CCACTGGGTTCCCAACATGGAATGCGCCCTTTTGGAACTGTGCGCATAGGTGATGTGCC 16396  
b 16081 CCACTGGGTTCCCAACATGGAATGCGCCCTTTTGGAACTGTGCGCATAGGTGATGTGCC 16140  
y 16397 GAGCGAGGGCTCTGATGAGCTTACGCCCATCAAGATCTTGAAAGGAGCGTGTATGTC 16456  
b 16141 GAGCGAGGGCTCTGATGAGCTTACGCCCATCAAGATCTTGAAAGGAGCGTGTATGTC 16200  
y 16457 CAGGACGAGATGTGAGCTGACGCTGTGGAGAAACGTGTGCTGGCGCTGGGGGGCCGG 16516  
b 16201 CAGGACGAGATGTGAGCTGACGCTGTGGAGAAACGTGTGCTGGCGCTGGGGGGCCGG 16260  
y 16517 GGTCTGCGGGCGGGCCCACTTCTCACCCAGTCCACTCCACTTCCAGACCCCGGTA 16576  
b 16261 GGTCTGCGGGCGGGCCCACTTCTCACCCAGTCCACTCCACTTCCAGACCCCGGTA 16320  
y 16577 AGGATGAGGGGGCGGAGCTGTCTCGGGCCCTGCTTATCCAGTTCAGCATCTGC 16636  
b 16321 AGGATGAGGGGGCGGAGCTGTCTCGGGCCCTGCTTATCCAGTTCAGCATCTGC 16380  
y 16637 GTTGGGATTTCTGAGTTTAGGGCGAGCAAGAGAACTTTGTGCTCTCTGAGTGGGCGAGGC 16696  
b 16381 GTTGGGATTTCTGAGTTTAGGGCGAGCAAGAGAACTTTGTGCTCTCTGAGTGGGCGAGGC 16440  
y 16697 CAGCGGATTTCTCTCAGGGGGCGTGGCCGGGGGGGCTCTTGGGGGGCGTGGCCAG 16756  
b 16441 CAGCGGATTTCTCTCAGGGGGCGTGGCCGGGGGGGCTCTTGGGGGGCGTGGCCAG 16500  
y 16757 GCGAAGGACTCATCGGGGGCGTGGCCAGCGGAGGGGCTCAAGAGGCGAGGCGCGG 16816  
b 16501 GCGAAGGACTCATCGGGGGCGTGGCCAGCGGAGGGGCTCAAGAGGCGAGGCGCGG 16560  
y 16817 TGGAGGGCTCTCTCGGGGGCGTGGCCAGCTGAGGGAATCTATCGGGGGCGTGGCCAGGCA 16876  
b 16561 TGGAGGGCTCTCTCGGGGGCGTGGCCAGCTGAGGGAATCTATCGGGGGCGTGGCCAGGCA 16620  
y 16877 GAGGGCTCTTTCGGGGCGTGGTCAGCGGATGAAATCTTTTGGGGGGGCTGGTTAGAGG 16936  
b 16621 GAGGGCTCTTTCGGGGCGTGGTCAGCGGATGAAATCTTTTGGGGGGGCTGGTTAGAGG 16680  
y 16937 GCGGGCTTTGTTCAGGCGATGGGATCAATATAGGCGTGGCCAGGAGATTTGGCTCCTTG 16996  
b 16681 GCGGGCTTTGTTCAGGCGATGGGATCAATATAGGCGTGGCCAGGAGATTTGGCTCCTTG 16740  
y 16997 GGGCGAGCGCAGGCGAGATATCAATGAGCGTATCCAGGCGAGTATCTTCGG 17056  
b 16741 GGGCGAGCGCAGGCGAGATATCAATGAGCGTATCCAGGCGAGTATCTTCGG 16800  
y 17057 AGGGCGTGGTCGGGCGATGAGCTCTCTCGGGGGCGTGGCCAGGCGGTGAGTTCCTCGGTG 17116

Db 16801 AGGGCGTGGTCGGGCGGATGAGCTCTCTCGGGGGCGTGGCCAGGCGGTGAGTTCTCGGTG 16860  
Qy 17117 GCATGGCTGGCCAGGTGAATGGTCTCTGGGAGGTCTGCTGAAGCGGTTCAGTTCTCTTG 17176  
Db 16861 GCATGGCTGGCCAGGTGAATGGTCTCTGGGAGGTCTGCTGAAGCGGTTCAGTTCTCTTG 16920  
Qy 17177 GGGCGTGGCCAGGTGAATGGTCTCTGGGGGAGTGGCCAGATGCTCTTCTCTCTCTGGG 17236  
Db 16921 GGGCGTGGCCAGGTGAATGGTCTCTGGGGGAGTGGCCAGATGCTCTTCTCTCTCTGGG 16980  
Qy 17237 AGCTTGTCTTGAAGTGGCTGTAGCCAGTGTCTCGAAATTTTTCAGAAAGGGGCGACAGTGG 17296  
Db 16981 AGCTTGTCTTGAAGTGGCTGTAGCCAGTGTCTCGAAATTTTTCAGAAAGGGGCGACAGTGG 17040  
Qy 17297 AGGAGGTGCTCTTCTAGTGGGCTGCGCCAGAAATGGGCTCCGAGTGCAGGGGTATCCAC 17356  
Db 17041 AGGAGGTGCTCTTCTAGTGGGCTGCGCCAGAAATGGGCTCCGAGTGCAGGGGTATCCAC 17100  
Qy 17357 TTTTGGATTTCTGACTGAAGGACACATCAGAAACAGGACATTTATTTCTTAGGATTCGAC 17416  
Db 17101 TTTTGGATTTCTGACTGAAGGACACATCAGAAACAGGACATTTATTTCTTAGGATTCGAC 17160  
Qy 17417 TTAGGGCGAGAGTCAAGAACCTGCAAGATTTTAAAGGGGCTGACTTTACTTCCAGGG 17476  
Db 17161 TTAGGGCGAGAGTCAAGAACCTGCAAGATTTTAAAGGGGCTGACTTTACTTCCAGGG 17220  
Qy 17477 CTCCGAATGAGAGTGGCCAGCCACTGATTTAAATATATATGATGAGCAACTTTGATTC 17536  
Db 17221 CTCCGAATGAGAGTGGCCAGCCACTGATTTAAATATATATGATGAGCAACTTTGATTC 17280  
Qy 17537 TTTTGGATTTTGAAGGAGTGTAGCTTTGTGTCCTCCAGGCTGGAGTGCATGCGCGA 17596  
Db 17281 TTTTGGATTTTGAAGGAGTGTAGCTTTGTGTCCTCCAGGCTGGAGTGCATGCGCGA 17340  
Qy 17597 TCTCGCTCTCACTGCAACTCGGCTCCGGGTTTAAAGCAATTTCTCCGCTCTCAGGCTCCT 17656  
Db 17341 TCTCGCTCTCACTGCAACTCGGCTCCGGGTTTAAAGCAATTTCTCCGCTCTCAGGCTCCT 17400  
Qy 17657 GAGTAGCTGGGATTTACAGGCTCCCGCCACACACTCAGCTGATTTTGTATTTTAGTAG 17716  
Db 17401 GAGTAGCTGGGATTTACAGGCTCCCGCCACACACTCAGCTGATTTTGTATTTTAGTAG 17460  
Qy 17717 AGACCGGGTTTTCGCCACGTTTGGCCAGGCTGGTCTGGAATCTCTGACCTCAGGTGATCCAC 17776  
Db 17461 AGACCGGGTTTTCGCCACGTTTGGCCAGGCTGGTCTGGAATCTCTGACCTCAGGTGATCCAC 17520  
Qy 17777 CCGCTTCGGCTCCCAAGTCTGGGATTTACGGCTGACGGCTGACCCACCGCCAGCTGCAAC 17836  
Db 17521 CCGCTTCGGCTCCCAAGTCTGGGATTTACGGCTGACGGCTGACCCACCGCCAGCTGCAAC 17580  
Qy 17837 TTTGATTTTAGTAGGAGCCAGAAATGTCATCTGTGTGAGTGGCTGTGGAAGAGATTT 17896  
Db 17581 TTTGATTTTAGTAGGAGCCAGAAATGTCATCTGTGTGAGTGGCTGTGGAAGAGATTT 17640  
Qy 17897 TTGTGTTCGGATTTTCAGAGCAATGGTGGGCTTCAGTCTTCAATTTCTGAGAGGCGGG 17956  
Db 17641 TTGTGTTCGGATTTTCAGAGCAATGGTGGGCTTCAGTCTTCAATTTCTGAGAGGCGGG 17700  
Qy 17957 GCCAAGACAGTGGTCTGATAGTTGGCGGTGTCTGCGGGTGGAGATTTCTGAGTAGCA 18016  
Db 17701 GCCAAGACAGTGGTCTGATAGTTGGCGGTGTCTGCGGGTGGAGATTTCTGAGTAGCA 17760  
Qy 18017 GGATTAGCACTTAGGGCCCTCCAGGATGTGGCTAGGTGCTCTGAATTTCTGTTGGG 18076  
Db 17761 GGATTAGCACTTAGGGCCCTCCAGGATGTGGCTAGGTGCTCTGAATTTCTGTTGGG 17820  
Qy 18077 TGCATCTGGAACCTTCCAGCTGTCTGAGTGTATCAGGAAAGAAATTTCTCTACTCTGG 18136  
Db 17821 TGCATCTGGAACCTTCCAGCTGTCTGAGTGTATCAGGAAAGAAATTTCTCTACTCTGG 17880  
Qy 18137 GTAGATGGATCCGCTCTTAAGCCCATGCACTTCTCCGAGGACCGCTGTATTTCTGTA 18196  
Db 17881 GTAGATGGATCCGCTCTTAAGCCCATGCACTTCTCCGAGGACCGCTGTATTTCTGTA 17940

18197	TGGAGTACGTCA	18256	19277	TCAGGAGTTTGAGA	19336	
17941	TGGAGTACGTCA	18000	Db	19021	TCAGGAGTTTGAGA	19080
18257	AGCCCCATGCA	18316	y	19337	AAATTTAGCCGG	19396
18001	AGCCCCATGCA	18060	Db	19081	AAATTTAGCCGG	19140
18317	GATCCAGCCAC	18376	y	19397	GAGAATCGCTTG	19456
18061	GATCCAGCCAC	18120	Db	19141	GAGAATCGCTTG	19200
18377	GAAATCGCTAT	18436	y	19457	CGAGCTGGGTG	19516
18121	GAAATCGCTAT	18180	Db	19201	CGAGCTGGGTG	19260
18437	CCAGGAATTTCC	18496	y	19517	GCCGGTGCAGTG	19576
18181	CCAGGAATTTCC	18240	Db	19261	GCCGGTGCAGTG	19320
18497	CTAGACTGTCTG	18556	y	19577	ACAAGTCCAGG	19636
18241	CTAGACTGTCTG	18300	Db	19321	ACAAGTCCAGG	19380
18557	GACCTGAAGCT	18616	y	19637	ATACAAAAATTA	19696
18301	GACCTGAAGCT	18360	Db	19381	ATACAAAAATTA	19440
18617	GGCATGTGTAA	18676	y	19697	AGGCAGGAGAA	19756
18361	GGCATGTGTAA	18420	Db	19441	AGGCAGGAGAA	19500
18677	GACTACATAGC	18736	y	19757	TGCACCTCCAG	19816
18421	GACTACATAGC	18480	Db	19501	TGCACCTCCAG	19560
18737	TAGAGGCTGAT	18796	y	19817	AGAAAAAGGCG	19876
18481	TAGAGGCTGAT	18540	Db	19561	AGAAAAAGGCG	19620
18797	TCATGAGTTGT	18856	y	19877	TTTTAAGTGGG	19936
18541	TCATGAGTTGT	18600	Db	19621	TTTTAAGTGGG	19680
18857	TTGGCACTGAG	18916	y	19937	TACGTATAGAT	19996
18601	TTGGCACTGAG	18660	Db	19681	TACGTATAGAT	19740
18917	CCTGTGGGTGA	18976	y	19997	CTCGTGCCCAA	20056
18661	CCTGTGGGTGA	18720	Db	19741	CTCGTGCCCAA	19800
18977	ACCCCTGGATC	19036	y	20057	GTAGAAAAATTT	20116
18721	ACCCCTGGATC	18780	Db	19801	GTAGAAAAATTT	19860
19037	TGTCCTCCGCA	19096	y	20117	GGGAAGCTGAGG	20176
18781	TGTCCTCCGCA	18840	Db	19861	GGGAAGCTGAGG	19920
19097	GCTCTCCCTGG	19156	y	20177	GGTGAAACCCCG	20236
18841	GCTCTCCCTGG	18900	Db	19921	GGTGAAACCCCG	19980
19157	GATGTAAGTGT	19216	y	20237	TCAACCCAGCTA	20296
18901	GATGTAAGTGT	18960	Db	19981	TCAACCCAGCTA	20040
19217	GGTGGCTCAC	19276	y	20297	TGCAGTGGAGCA	20356
18961	GGTGGCTCAC	19020	Db	20041	TGCAGTGGAGCA	20100
			y	20357	TCAAAAAGAAAA	20416







QY	22577	TAGCCTCCCTTCGATGGGAGGACGAGGAGGCTGTTTTCAGGCCATCATGGAACAACT	22636
DB	22321	TAGCCTCCCTTCGATGGGAGGACGAGGAGGCTGTTTTCAGGCCATCATGGAACAACT	22380
QY	22637	GTCACTACCCCAAGTCGCTTTCCCGGAAGCCGCTGGCCATCTGCAAGGGGGTGAGAGCC	22696
DB	22381	GTCACTACCCCAAGTCGCTTTCCCGGAAGCCGCTGGCCATCTGCAAGGGGGTGAGAGCC	22440
QY	22697	CCCTGACTCCAGCTTCTCCAGGCTCA CAACACACACCCCATCTGCTCTCTGTCGCTA	22756
DB	22441	CCCTGACTCCAGCTTCTCCAGGCTCA CAACACACACCCCATCTGCTCTCTGTCGCTA	22500
QY	22757	TTAGAAAATGCTCCCATCTGTAAGTCACTTACTTCCATCTGTTGAAAAGTTGATAT	22816
DB	22501	TTAGAAAATGCTCCCATCTGTAAGTCACTTACTTCCATCTGTTGAAAAGTTGATAT	22560
QY	22817	GATGATAGGTTTGTAGAAATGATTTCCAGCCCTGTTGCCACAGAGGCTCGAGATG	22876
DB	22561	GATGATAGGTTTGTAGAAATGATTTCCAGCCCTGTTGCCACAGAGGCTCGAGATG	22620
QY	22877	GCCTCTGTCTCATCTTCTCTGTGACTCCCACTCCCAAGCTCCCTGCTGTGAGGAAGTGC	22936
DB	22621	GCCTCTGTCTCATCTTCTCTGTGACTCCCACTCCCAAGCTCCCTGCTGTGAGGAAGTGC	22680
QY	22937	TGAAAAGTCAGGGTGTCTGTCTGTAGAACTGGGTGGGTGAGTAAACCAACTTCTGC	22996
DB	22681	TGAAAAGTCAGGGTGTCTGTCTGTAGAACTGGGTGGGTGAGTAAACCAACTTCTGC	22740
QY	22997	AGCTTTTCTCTGCTGTGAACTTTGGGTGAGTCACCAAACTTTGTGAGCTTAACTCTCTT	23056
DB	22741	AGCTTTTCTCTGCTGTGAACTTTGGGTGAGTCACCAAACTTTGTGAGCTTAACTCTCTT	22800
QY	23057	CAGGGGTTATGAGGTTGACAGAAAGAACCTTGCGCCATAGCAGATTTTCAGGCCCAT	23116
DB	22801	CAGGGGTTATGAGGTTGACAGAAAGAACCTTGCGCCATAGCAGATTTTCAGGCCCAT	22860
QY	23117	GTACGACCTTCTGGGTCTAGTGTCTCTGTGATCTCCCTGACAGTCTCTCTGGTTTC	23176
DB	22861	GTACGACCTTCTGGGTCTAGTGTCTCTGTGATCTCCCTGACAGTCTCTCTGGTTTC	22920
QY	23177	TGCTCATGCTCCCTCCATCTGATACGATGGGGCTCTCTGTGTTTCTTCTTCTTCTC	23236
DB	22921	TGCTCATGCTCCCTCCATCTGATACGATGGGGCTCTCTGTGTTTCTTCTTCTTCTC	22980
QY	23237	TGTGTCTCTTCTGCATCTGTCTACACTTTTGGGCTTTGTTCACACCCCTTACCCCC	23296
DB	22981	TGTGTCTCTTCTGCATCTGTCTACACTTTTGGGCTTTGTTCACACCCCTTACCCCC	23040
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DB	23101	CTGCTGGCTTTCTGCTCCCTCTTCTCTGGGTCTCTGTGCCCATATTTGGTCTTTATTC	23160
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DB	23221	CCTGGGTCTCTCTGCTCTCCCTCTCTGAGTTTCTGAGTTTCTTACCTGGGGTCTCTG	23280
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DB	23281	TACCAACCTCTGAAATTTCTATTTCCCTTTTCTCTGGGTCTGCAACCTCTCTTCCCTCC	23340
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DB	23341	TCCCTCCCTCTTCCCTCTCATCTCTACCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT	23400

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DB	23641	GTCTCTCTCTCTCTGTGCTC	23700
QY	23957	TCTCTGTC	24016
DB	23701	TCTCTGTC	23760
QY	24017	CT	24076
DB	23761	CT	23820
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DB	23941	CTCTGGGTCTACCTGTCCGGCACTCTGTCTGTGTTGTCTGTCTCTCTCTCTCTCTCTCT	24000
QY	24257	CACAGTTCTTGACCAAGCACCCAGGAGCGCTGGGCTCAGAGCCCTGATGGGGAACCTA	24316
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13364	TAGAGCTCAGTGAGCGCAGATCGCTCCACTGCCTCCAGCTGGATCAGAGGGAGA	13423	Y				
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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

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Searched: 1 seqs, 169997 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : ac008440.ig.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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DOE Joint Genome Institute and Stanford Human Genome Center.  
AUTHORS Direct Submission  
TITLE Unpublished  
JOURNAL  
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AUTHORS Direct Submission  
TITLE Direct Submission  
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REFERENCE 3 (bases 1 to 169997)  
DOE Joint Genome Institute and Stanford Human Genome Center.  
AUTHORS Direct Submission  
TITLE Direct Submission

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DOE Joint Genome Institute and Stanford Human Genome Center.  
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www.shgc.stanford.edu  
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DB 26480 TCTCCGGAGGGAGCGCTTTAAGCCGAAACCCCGCCCTCTCGTCTCTCTGGCAAGC 26539  
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Search completed: October 20, 2006, 10:08:12

Job time : 3392 secs





GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: October 20, 2006, 09:20:33 ; Search time 3681 Seconds  
(without alignments)  
2.615 Million cell updates/sec

Title: US-10-671-007-3  
Perfect score: 25301  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 190210 residues  
Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : ac022318.ig:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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2	773.299	3.1	190210	1	ac022318

# ALIGNMENTS

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DEFINITION Homo sapiens chromosome 19 clone RP11-158G19, WORKING DRAFT  
SEQUENCE, 16 unordered pieces.  
ACCESSION AC022318  
VERSION AC022318.5 GI:15321555  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 190210)  
Waterston,R.H.  
The sequence of Homo sapiens clone  
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Waterston,R.H.  
Direct Submission  
Submitted (30-JAN-2000) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
On Aug 28, 2001 this sequence version replaced gi:8516165.

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc/index.shtml  
----- Project Information -----  
Center project name: H.NH0158G19  
----- Summary Statistics -----  
Sequencing vector: M13, 64%  
Chemistry: Dye-terminator ET; 64% of reads  
Chemistry: Dye-terminator Big Dye; 36% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 179489 bases at least Q40  
Consensus quality: 183023 bases at least Q30  
Consensus quality: 184976 bases at least Q20  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 16 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence.  
\* as soon as it is available and the accession number will  
\* be preserved.  
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\* 3107: contig of 1978 bp in length  
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; AUTHORS Waterston,R.H.
; TITLE Direct Submission
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; University School of Medicine, 444 Forest Park Parkway, St. Louis,
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; NOTE: This is a 'working draft' sequence. It currently
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; arbitrary. Gaps between the contigs are represented as
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; This record will be updated with the finished sequence
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Qy	10405	GGGAGCCATGAGCTCGGCTCTGCACCCCATCCACCCCACTTCTTCGACAGCAACTGAGC	10464
Db	59103	TAGGCACAGTGGCTTTACACTGTAAATCCACGACACTTTGGAGGGCTGAGGTGGCGGATCA	59162
Qy	10465	CAGGGGATGTGGAGCGCGGCTCAGCGTGGAGGTGTGGACTCTGGGACCTGGGACCGGACCT	10524

[illegible]



Qy	13554	GGG-----GTTCCACCTGCATCAGAAATTCCTAGAGTGCTTGTCTTTTAAAGC	13599
Db	62167	AGGAGAAAAACGAAATCATCTCATGCCCATGAACCTCCTCTTGGGCTATGTGAAGGGG	62226
Qy	13600	ACATTCCCCAGCCTTTCTGCAGACCTACTCAGTGACGATCTCTGTGATGCCCTCAAATGTC	13659
Db	62227	AATTCCTGAGGGTCTCTTTGCCATGCAGCAGGAGAGCCTCTGGCTGTGGTGGCTCTTGT	62286
Qy	13660	TGCCTACTAAATTAATTCCTCAGGTGATCCTTTTGCAAGTTAAGTTTGAGATGGGCTC	13719
Db	62287	TGGATCCAAGAGCA-----GAGGAGGAATGTGTGAAGGACTTTGAGTAAAGCAA	62338
Qy	13720	TGCGCGCGGGCGAGTGGCTCACGCCCTGTATCCAGCACTTTGGGAGGCCAAGCGGGT	13779
Db	62339	AAGAGCCGGGCGCGGTGGCTCACGCCCTATATCCAGCACTTTGGGAGGCCGAGCGGGC	62398
Qy	13780	GGATCAGAGGTCAGGAGATCGAGACCATCTGGCTAACACGGTGAATCCCGCTCTCTAC	13839
Db	62399	GGATCAGAGGTCAGGAGATCGAGACCATCTGGCTAACATGCTGAACCCCGTCTCTAC	62458
Qy	13840	TAAAAATACAAAAAATTAGTGGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	13899
Db	62459	TAAAAATAC-AAAAAATTAGCCAGCGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	62517
Qy	13900	GAGGCTGAGGCGAGGAATGGCATGAACCTGGGAGTGGAGCTTGGCAATGAGCCGAGATC	13959
Db	62518	GAGGCTGAGGCGAGGAATGGCTGMAACCCGGGAGGAGAGCTTGCAGTGAGCAGAGATA	62577
Qy	13960	GTGCCACTGCACTACAGCCTGGGTGACAGCGAGACTCTATCTCAGAAAAAAGAAAAA	14019
Db	62578	GAGCCTGCACTCCAGCCTGGGTGACAGCGAGACTCCCTCTCAAAAAAAGAAAAAAG	62637
Qy	14020	AGAGAGA	14026
Db	62638	CAGNAGA	62644

Search completed: October 20, 2006, 10:23:51  
Job time : 3797 secs



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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:      October 20, 2006, 09:22:48 ; Search time 420 Seconds
              (without alignments)
              2.988 Million cell updates/sec

Title:      US-10-671-007-3
Perfect score: 25301
Sequence: 1 agcccccgaagctgagttat.....tactttacatgaatggaga 25301

```

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 24801 residues  
Total number of hits satisfying chosen parameters: 2

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : abz20990:★

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24801	98.0	24801	1	Human thyroid tumor
2	576.397	2.3	24801	1	Human thyroid tumor

## ALIGNMENTS

RESULT 1	
ABZ20990	
ID	ABZ20990 standard; DNA; 24801 BP.
XX	
XX	ABZ20990;
XX	
XX	AC
XX	AC
DT	10-APR-2003 (first entry)
XX	
XX	Human thyroid tumour associated PKCG genomic sequence SEQ ID NO: 18.
DE	
XX	Thyroid; cancer; hyperplasia; human; chromosome 19q13; CAT; DC2;
KW	PKCgamma; PKCG; cytostatic; antithyroid; gene; ds.
KW	
XX	
XX	
OS	Homo sapiens.
XX	
XX	WO200283727-A2.
PN	
XX	
PD	24-OCT-2002.
XX	
XX	12-APR-2002; 2002WO-EP004090.
PF	
XX	
XX	12-APR-2001; 2001DE-01018452.
PR	
XX	
XX	(BULL/) BULLERDIEK J.
PA	
XX	
PI	Bullerdiek J;







Db 7321 CCCCAGGACCCCGGAACAAACAAAGTTCCGCTCGCATAGCTACAGAGCCGCCACCTTC 7380  
Qy 7637 TGGGACCATGTGGCTCCCTCTCTAGCGGCTTGTGCACAGGCGATGAAATGCTCTGT 7696  
Db 7381 TGGGACCATGTGGCTCCCTCTCTAGCGGCTTGTGCACAGGCGATGAAATGCTCTGT 7440  
Qy 7697 GAGTGACCTGGGCTTGGCCAGGCGCTTCCAAAGCGCCGCTGTGGGTTCCGGGAATGC 7756  
Db 7441 GAGTGACCTGGGCTTGGCCAGGCGCTTCCAAAGCGCCGCTGTGGGTTCCGGGAATGC 7500  
Qy 7757 CCGGATGGGGTGGGGTGGAGTCTTGGCTTGGGGCGGGGCTCGAGTGTCTACCCGCA 7816  
Db 7501 CCGGATGGGGTGGGGTGGAGTCTTGGCTTGGGGCGGGGCTCGAGTGTCTACCCGCA 7560  
Qy 7817 GCTTTCCCTCCAGGCTCGAGATGAACGTGACCGGCGCTGTGGTGTGGGCTC 7876  
Db 7561 GCTTTCCCTCCAGGCTCGAGATGAACGTGACCGGCGCTGTGGTGTGGGCTC 7620  
Qy 7877 CTTGTCGGTGTGGACACACAGCGCGCGCGGCGCTGCGAGTCCGGGCTCC 7936  
Db 7621 CTTGTCGGTGTGGACACACAGCGCGCGCGGCGCTGCGAGTCCGGGCTCC 7680  
Qy 7937 CACAGCAGATGAGATCCAGTAACTGGTGAAGGCCCGCCCTCGCTCGCCCGCGCC 7996  
Db 7681 CACAGCAGATGAGATCCAGTAACTGGTGAAGGCCCGCCCTCGCTCGCCCGCGCC 7740  
Qy 7997 TCCCAAGTGTGAGCGGGCTGACCCAAAGGCACTTGTGCTGGCCCGAGCTTACCCCAA 8056  
Db 7741 TCCCAAGTGTGAGCGGGCTGACCCAAAGGCACTTGTGCTGGCCCGAGCTTACCCCAA 7800  
Qy 8057 GATGGGCGCAGCTCTTCTATGCTGACGCCACACTCTGACCCCGCCCGCCCGCGCG 8116  
Db 7801 GATGGGCGCAGCTCTTCTATGCTGACGCCACACTCTGACCCCGCCCGCCCGCGCG 7860  
Qy 8117 AGCACACCCAGCATACCCCTTTTGGCTCGAAGCCCGCGCTCCAACTGGCTTCTTGCAA 8176  
Db 7861 AGCACACCCAGCATACCCCTTTTGGCTCGAAGCCCGCGCTCCAACTGGCTTCTTGCAA 7920  
Qy 8177 CTTTCTGACCTGTTAATGACTTGTCTTTTGGGACGAGTTTGGCTCT 8236  
Db 7921 CTTTCTGACCTGTTAATGACTTGTCTTTTGGGACGAGTTTGGCTCT 7980  
Qy 8237 TGTGCTCAAGCTGAGTGAATGGCGCATCTCGGCTCACTGCACTTCCGCTCCCG 8296  
Db 7981 TGTGCTCAAGCTGAGTGAATGGCGCATCTCGGCTCACTGCACTTCCGCTCCCG 8040  
Qy 8297 GTTCAAGTGATTTCTCTGCTCAGCCTCCCGAGTAGCTGGGATTAAGCGGCTGCACC 8356  
Db 8041 GTTCAAGTGATTTCTCTGCTCAGCCTCCCGAGTAGCTGGGATTAAGCGGCTGCACC 8100  
Qy 8357 AAGCCGGCTAATTTTGTATTTTGTATACAAAGGGGTTTCAATGTTAGCAGGCT 8416  
Db 8101 AAGCCGGCTAATTTTGTATTTTGTATACAAAGGGGTTTCAATGTTAGCAGGCT 8160  
Qy 8417 GCTCTGAACTCTGACCCAGGTGATCCCTCGACTCGGCTCCCAAGTCTGGATT 8476  
Db 8161 GCTCTGAACTCTGACCCAGGTGATCCCTCGACTCGGCTCCCAAGTCTGGATT 8220  
Qy 8477 AACAGCGTGAAGCCAGCGGCTTGGCCAAATGGCTTTTGTATTTTGTATTTT 8536  
Db 8221 AACAGCGTGAAGCCAGCGGCTTGGCCAAATGGCTTTTGTATTTTGTATTTT 8280  
Qy 8537 ATTTTGTGAGATGAGTCTTGTCTGTCAACGAGCTGGAGTGCAGTGCATCTTG 8596  
Db 8281 ATTTTGTGAGATGAGTCTTGTCTGTCAACGAGCTGGAGTGCAGTGCATCTTG 8340  
Qy 8597 GCTCACTGAATCTTGCCTCCGGGTTCAAGGGATTTCCCTGACCTCCCGAGTA 8656  
Db 8341 GCTCACTGAATCTTGCCTCCGGGTTCAAGGGATTTCCCTGACCTCCCGAGTA 8400  
Qy 8657 GCTGGAATTAACAGGCGCTTGCACACATCCGGCTAAATTTTGTGAGTCTGGGGTGCAGGAA 8716

Db 8401 GCTGGAATTAACAGGCGCTTGCACACATCCGGCTAAATTTTGTGAGTCTGGGGTGCAGGAA 8460  
Qy 8717 GACRAGATCTCGCTCTGTTGCCAGGCTGGAGTGCAGTAGCATGATCTCAGCTCACTGA 8776  
Db 8461 GACAAAGATCTCGCTCTGTTGCCAGGCTGGAGTGCAGTAGCATGATCTCAGCTCACTGA 8520  
Qy 8777 ACTTCGGCTCTCAGGTTCAAGCGATTTCTCTGCTTCAGCTTCTCAGTAGCTGGGACTA 8836  
Db 8521 ACTTCGGCTCTCAGGTTCAAGCGATTTCTCTGCTTCAGCTTCTCAGTAGCTGGGACTA 8580  
Qy 8837 CAGGTGCATGACACATGACACCGAGCTCATTTTGTATTTTGTATAGTAGAGAGGTTTCA 8896  
Db 8581 CAGGTGCATGACACATGACACCGAGCTCATTTTGTATTTTGTATAGTAGAGAGGTTTCA 8640  
Qy 8897 ATGCTAGCACGCTGCTTGGAACTCTGACCTCAGGTGATCCGCGCTCCGCTCC 8956  
Db 8641 ATGCTAGCACGCTGCTTGGAACTCTGACCTCAGGTGATCCGCGCTCCGCTCC 8700  
Qy 8957 AAAGTGTCTGGGATTAACAGGCTGAGGACCGTCCCGGCAATGGCTTTCTGGGTATAAGCA 9016  
Db 8701 AAAGTGTCTGGGATTAACAGGCTGAGGACCGTCCCGGCAATGGCTTTCTGGGTATAAGCA 8760  
Qy 9017 TCTTGAGAAAGGAGATACCTGGTCTCAGGAGGCTGTGGTTCAGTACTGTGTGACATGG 9076  
Db 8761 TCTTGAGAAAGGAGATACCTGGTCTCAGGAGGCTGTGGTTCAGTACTGTGTGACATGG 8820  
Qy 9077 CCAGGCTCCAACTCTGCTTCTAATGAGAGAGGCTCTGGATCTGATTTTCAAGGTTCA 9136  
Db 8821 CCAGGCTCCAACTCTGCTTCTAATGAGAGAGGCTCTGGATCTGATTTTCAAGGTTCA 8880  
Qy 9137 CTGTTGCGGAAAGGCTCTATGCTCTCTGCTTCTGGGTTCTGGAGAGTAAAGTCAATG 9196  
Db 8881 CTGTTGCGGAAAGGCTCTATGCTCTCTGCTTCTGGGTTCTGGAGAGTAAAGTCAATG 8940  
Qy 9197 AGAAACAGACTGAGAGCTTGGAACTCTTTTGTGAGAGAGGAGTCTCGCTG 9256  
Db 8941 AGAAACAGACTGAGAGCTTGGAACTCTTTTGTGAGAGAGGAGTCTCGCTG 9000  
Qy 9257 TGAGCCCGAGCTGGAGTGCAGTGCCTGCTGCTGCTCACTGCAAGCTCCGACTCTG 9316  
Db 9001 TGAGCCCGAGCTGGAGTGCAGTGCCTGCTGCTGCTCACTGCAAGCTCCGACTCTG 9060  
Qy 9317 GTTCAAGCTCATTTCTCCGCTCAGCTCTCAGTAGCTGGGACCAAGAGTCTCCGCTC 9376  
Db 9061 GTTCAAGCTCATTTCTCCGCTCAGCTCTCAGTAGCTGGGACCAAGAGTCTCCGCTC 9120  
Qy 9377 ACGCCAGCTAATTTTGTATTTTGTATTTTGTATTTTGTATTTTGTATTTTGTATTTT 9436  
Db 9121 ACGCCAGCTAATTTTGTATTTTGTATTTTGTATTTTGTATTTTGTATTTTGTATTTT 9180  
Qy 9437 CAGGATGCTCGATCTCCTGACCTTGTGATCCGCGCTTGGCTCCCAAGTGTG 9496  
Db 9181 CAGGATGCTCGATCTCCTGACCTTGTGATCCGCGCTTGGCTCCCAAGTGTG 9240  
Qy 9497 GATTACAGCATGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 9556  
Db 9241 GATTACAGCATGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 9300  
Qy 9557 GAGGCTGGGAGCGCTTCTGATCTCTAAACCGCTGACCTCTTCTCTCTCTCTCTCTCTCT 9616  
Db 9301 GAGGCTGGGAGCGCTTCTGATCTCTAAACCGCTGACCTCTTCTCTCTCTCTCTCTCTCT 9360  
Qy 9617 AGTTGGGAGCGCTTCTGATCTCTAAATTTCTGAGCCCAATGCTCTCTGATCTCTCTG 9676  
Db 9361 AGTTGGGAGCGCTTCTGATCTCTAAATTTCTGATCCCAATGCTCTCTGATCTCTCTG 9420  
Qy 9677 GAACTGAAGCTCATCCAGACCTCGGAACCTGACGAAACAGAGACCCGAGTGA 9736  
Db 9421 GAACTGAAGCTCATCCAGACCTCGGAACCTGAGCAAGAGACCCGAGTGA 9480  
Qy 9737 AGCCAGCTAAACCTGTGTGAGTGAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9796  
Db 9481 AGCCAGCTAAACCTGTGTGAGTGAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9540

QY	9797	GGCAATGACACCTGACAGAGAAATGATCTGAGGGTCTTAGTGGCCCCCAGAGAGCAGCTGA	9856
DB	9541	GGCAATGACACCTGACAGAGAAATGATCTGAGGGTCTTAGTGGCCCCCAGAGAGCAGCTGA	9600
QY	9857	TGGGAGGGGTTAGGATAGAGAGAAACCCAGAAAGGGCAGAAAGATGCTGGGAAAGGG	9916
DB	9601	TGGGAGGGGTTAGGATAGAGAGAAACCCAGAAAGGGCAGAAAGATGCTGGGAAAGGG	9660
QY	9917	AATAGAGTGTAGAGGGAGTGGGATGGAGATACAGAAACGGAGAGACAGCCAGACCACTG	9976
DB	9661	AATAGAGTGTAGAGGGAGTGGGATGGAGATACAGAAACGGAGAGACAGCCAGACCACTG	9720
QY	9977	TATTAATAGTCTCCATTGAAGCCCCACCTTTAGAGTTAGACAGATGAGAGAGAGAG	10036
DB	9721	TATTAATAGTCTCCATTGAAGCCCCACCTTTAGAGTTAGACAGATGAGAGAGAGAG	9780
QY	10037	AGAGAGTCTCAGAGAGAGCAGAAACCCAGAGAGAGACACAGATGGAGAGGGAGAGAA	10096
DB	9781	AGAGAGTCTCAGAGAGAGCAGAAACCCAGAGAGAGACACAGATGGAGAGGGAGAGAA	9840
QY	10097	GATGGGGATGGCAGGGAGACAGAGATCAGTTGACAGAGACAGAGATGATAGAGACCA	10156
DB	9841	GATGGGGATGGCAGGGAGACAGAGATCAGTTGACAGAGACAGAGATGATAGAGACCA	9900
QY	10157	GAGAGGAGAGAGGATCAGAGACTCAGAGAGAGAGATCTCGAGAGACAGAGACAGAG	10216
DB	9901	GAGAGGAGAGAGGATCAGAGACTCAGAGAGAGAGATCTCGAGAGACAGAGACAGAG	9960
QY	10217	TGGGAAAGGGCGGAGATGACAGGAGGAGGAGAGAGAGCTCTCTAGGTTTACTTTAG	10276
DB	9961	TGGGAAAGGGCGGAGATGACAGGAGGAGGAGAGAGAGCTCTCTAGGTTTACTTTAG	10020
QY	10277	GCCCAAGCCCTAGCTGGAGAGAGAGCCCGGCTGGGAGAGGTCTAGAGTGGAGACCGAC	10336
DB	10021	GCCCAAGCCCTAGCTGGAGAGAGAGCCCGGCTGGGAGAGGTCTAGAGTGGAGACCGAC	10080
QY	10337	AAAGCAGAGAGAGAGCCCGCTGGGTTGCCCCACCTCCAGCACCAAGGATGGG	10396
DB	10081	AAAGCAGAGAGAGAGCCCGCTGGGTTGCCCCACCTCCAGCACCAAGGATGGG	10140
QY	10397	GAACCGAGGGAGGCATGAGCTCGGCTCTGCACCCCATCCACCCCACTTCTGACAGAA	10456
DB	10141	GAACCGAGGGAGGCATGAGCTCGGCTCTGCACCCCATCCACCCCACTTCTGACAGAA	10200
QY	10457	CCTGAAGCCAGGGATGTGAGAGCCCGCTCAGCGTGGAGGTGGAGTGGGACCGGAC	10516
DB	10201	CCTGAAGCCAGGGATGTGAGAGCCCGCTCAGCGTGGAGGTGGGACCTGGGACCGGAC	10260
QY	10517	CTCCCGCAACGACTTCATGGGGGCCATGTCTTTGGGCTCTCGAGCTGCTCAAGGGGCC	10576
DB	10261	CTCCCGCAACGACTTCATGGGGGCCATGTCTTTGGGCTCTCGAGCTGCTCAAGGGGCC	10320
QY	10577	CGTGGATGGCTGGTCAGGAGCAGGGCTGGGGCTGGGGATGGAGCAATATTACCATCT	10636
DB	10321	CGTGGATGGCTGGTCAGGAGCAGGGCTGGGGCTGGGGATGGAGCAATATTACCATCT	10380
QY	10637	CCATCTGTGTGTCTCTCTCTCAGGCACTGTCTTCCCTCTGCTCCCTCCAGAGATGC	10696
DB	10381	CCATCTGTGTGTCTCTCTCTCAGGCACTGTCTTCCCTCTGCTCCCTCCAGAGATGC	10440
QY	10697	GCAC	10756
DB	10441	GCAC	10500
QY	10757	ATTCT	10816
DB	10501	ATTCT	10560
QY	10817	TCTCTTCCATCTGTGTGTCTCTCTGTGTCTCTCTTCTCTCTCTCTCTCTCTCTCT	10876
DB	10561	TCTCTTCCATCTGTGTGTCTCTCTGTGTCTCTCTTCTCTCTCTCTCTCTCTCTCT	10620

QY	10877	TCTCCCATGGTGGCCCCATCCCGCTGCGGCTCTGCTCTCGTCTGTATGTACAGGTAC	10936
DB	10621	TCTCCCATGGTGGCCCCATCCCGCTGCGGCTCTGCTCTCGTCTGTATGTACAGGTAC	10680
QY	10937	AAGTTACTGAACACAGGAGGAGGCGAGTATTAAATGTGCGCGGTGGCCGATGTGCAAC	10996
DB	10681	AAGTTACTGAACACAGGAGGAGGCGAGTATTAAATGTGCGCGGTGGCCGATGTGCAAC	10740
QY	10997	TGCAGCTCTCTCCAGAGTTGAGGTACCCAGACCTGCTTCTTCCCAAGGAGCCAGGCC	11056
DB	10741	TGCAGCTCTCTCCAGAGTTGAGGTACCCAGACCTGCTTCTTCCCAAGGAGCCAGGCC	10800
QY	11057	CAGCTCTCCACAGGTCAGAGCTGGCCCTTCTTCCCAAGGAGCCAGGCCCTGCTG	11116
DB	10801	CAGCTCTCCACAGGTCAGAGCTGGCCCTTCTTCCCAAGGAGCCAGGCCCTGCTG	10860
QY	11117	GACTACAGTTCCAGAGACCTTAGGACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT	11176
DB	10861	GACTACAGTTCCAGAGACCTTAGGACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT	10920
QY	11177	CCAGGCTCTGATGGGAATTAATAGTTCTCTATCTATGCGCCATGGCTTCTGAGGTACTAGGGGC	11236
DB	10921	CCAGGCTCTGATGGGAATTAATAGTTCTCTATCTATGCGCCATGGCTTCTGAGGTACTAGGGGC	10980
QY	11237	CACAGCCCTCTGTTAGGGCGATCCCTGCACTCTCTGGGACCTGACTCTCTCTCTCT	11296
DB	10981	CACAGCCCTCTGTTAGGGCGATCCCTGCACTCTCTGGGACCTGACTCTCTCTCTCT	11040
QY	11297	TTTCTCCAGGCTGTGAACTACCCCTGGAAATGATAGGTGAGTAGAACAGGGCGTT	11356
DB	11041	TTTCTCCAGGCTGTGAACTACCCCTGGAAATGATAGGTGAGTAGAACAGGGCGTT	11100
QY	11357	GATGAGGCGAGTTTCT	11416
DB	11101	GATGAGGCGAGTTTCT	11160
QY	11417	CAATTCCTCCACACATGAGTTGAGCACACATTTGTGCTAGGCTGTCTGTGCTGTGAA	11476
DB	11161	CAATTCCTCCACACATGAGTTGAGCACACATTTGTGCTAGGCTGTCTGTGCTGTGAA	11220
QY	11477	TAATCCAGGATCCAGAGATGAATCTGACCTCAAGCAACTCTCCAGGTAGGGACACAGT	11536
DB	11221	TAATCCAGGATCCAGAGATGAATCTGACCTCAAGCAACTCTCCAGGTAGGGACACAGT	11280
QY	11537	CACAGATCTTAAATACAGGAAGATGTCTAAATTAGAGGTAGCCAGGGCACTGAAGA	11596
DB	11281	CACAGATCTTAAATACAGGAAGATGTCTAAATTAGAGGTAGCCAGGGCACTGAAGA	11340
QY	11597	GGCTAACCGAGGCATAATCCAGCCTGGGGAGGTGTGAGGAGGACTTCCCTGAGG	11656
DB	11341	GGCTAACCGAGGCATAATCCAGCCTGGGGAGGTGTGAGGAGGACTTCCCTGAGG	11400
QY	11657	AGGTGAGCCTGAAATGATTTGAGGTTTAAATTTTAAATTTTAAATTTTAAATTTT	11716
DB	11401	AGGTGAGCCTGAAATGATTTGAGGTTTAAATTTTAAATTTTAAATTTTAAATTTT	11460
QY	11717	ATTTTATTTTATTTTCTGCGCCAGGCTGAGTGCATTTGGCACAAATCTCGCCTCACCTG	11776
DB	11461	ATTTTATTTTATTTTCTGCGCCAGGCTGAGTGCATTTGGCACAAATCTCGCCTCACCTG	11520
QY	11777	CAACCTCCAGCTCCCGGTTCAAGCAATTTCTTTGCTCAGCCTCTCTGAGTAGCTGGAT	11836
DB	11521	CAACCTCCAGCTCCCGGTTCAAGCAATTTCTTTGCTCAGCCTCTCTGAGTAGCTGGAT	11580
QY	11837	TACAGTGACCGCCACACACCCAGCTAAATTTTATTTTATTTTATTTTATTTTATTTT	11896
DB	11581	TACAGTGACCGCCACACACCCAGCTAAATTTTATTTTATTTTATTTTATTTTATTTT	11640
QY	11897	TGCGCAATGTGGCAGCTGATCTCAAACTCCCAAACTCAGGTGATCCGCTTGGC	11956
DB	11641	TGCGCAATGTGGCAGCTGATCTCAAACTCCCAAACTCAGGTGATCCGCTTGGC	11700
QY	11957	CTCCCAAGTGTGGGATTTACAGGCAATGAGCCACTGCGCCCGACCGATTTCTTGTGTTT	12016



[illegible]

Db	12781	CGTGGCTCTACTCACTCGGGGATATAGAGAAACGAGGAAAGAAACAAACAAACAAAA	1284
QY	13097	AAGTTCCCTTCTTATGGGATTTACACCGGGAGAGACATTAACAAAAATATAATAGCA	13156
Db	12841	AAGTTCCCTTCTTATGGGATTTACACCGGGAGAGACATTAACAAAAATATAATAGCA	12900
QY	13157	TATGATAGACTGGGCACGATGCCTCATGTCTGTGATCTTAGTAGCGCGGGATCACCT	13216
Db	12901	TATGATAGACTGGGCACGATGCCTCATGTCTGTGATCTTAGTAGCGCGGGATCACCT	12960
QY	13217	GAGGTCAGGAGTTTGAGACACGCTGGCCAGCGTGGCGAAACCCCATCTCTCTATAAAAA	13276
Db	12961	GAGGTCAGGAGTTTGAGACACGCTGGCCAGCGTGGCGAAACCCCATCTCTCTATAAAAA	13020
QY	13277	TACAAAAATCAGCTGGGCATGCTGGAGGCGCTGTAAATCCACGCTACTCGGAAGGCTGAG	13336
Db	13021	TACAAAAATCAGCTGGGCATGCTGGAGGCGCTGTAAATCCACGCTACTCGGAAGGCTGAG	13080
QY	13337	GCAGGAGAATTGCTGGATTTCCGGGAAGTAGAGGCTGCAGTGGAGCCAGATCGCTCCAATG	13396
Db	13081	GCAGGAGAATTGCTGGATTTCCGGGAAGTAGAGGCTGCAGTGGAGCCAGATCGCTCCAATG	13140
QY	13397	CACCTCCAGCTGGATGACAGAGGGAGACTCTGTCTCAAAAAAATAAAAAAAGAA	13456
Db	13141	CACCTCCAGCTGGATGACAGAGGGAGACTCTGTCTCAAAAAAATAAAAAAAGAA	13200
QY	13457	GACAGAAATCTTCAAGATTTCAACACAGCAACAAATGTTATAGTCTTTACTGGACTCTT	13516
Db	13201	GACAGAAATCTTCAAGATTTCAACACAGCAACAAATGTTATAGTCTTTACTGGACTCTT	13260
QY	13517	ACAGAAATCTTCAACAGAGTTTTTAATGTTGTGTGGGGTTTCACTGCATCAGAATTC	13576
Db	13261	ACAGAAATCTTCAACAGAGTTTTTAATGTTGTGTGGGGTTTCACTGCATCAGAATTC	13320
QY	13577	CTAGAGTCTTGCTTTTAAAAGCACATTTCCACAGCCTTTTCGCAGACCTACTCAGTGACG	13636
Db	13321	CTAGAGTCTTGCTTTTAAAAGCACATTTCCACAGCCTTTTCGCAGACCTACTCAGTGACG	13380
QY	13637	ATCTCTGTAGTCCTCAAAATGTCGCTACTAAATTAATTCCTCAGTGATCTCTTTTGCA	13696
Db	13381	ATCTCTGTAGTCCTCAAAATGTCGCTACTAAATTAATTCCTCAGTGATCTCTTTTGCA	13440
QY	13697	AAGTTAAGTTTGAGAAATGGGCTCTCGGCGCGGCGCAGTGGCTCAGCCCTGTATCCACG	13756
Db	13441	AAGTTAAGTTTGAGAAATGGGCTCTCGGCGCGGCGCAGTGGCTCAGCCCTGTATCCACG	13500
QY	13757	CATTTGGAGGCCAAGCGGGTGGATACGAGGTCGAGAGTCGAGACCATCCTGGCTA	13816
Db	13501	CATTTGGAGGCCAAGCGGGTGGATACGAGGTCGAGAGTCGAGACCATCCTGGCTA	13560
QY	13817	ACAGGTGAATCCCGTCTCTACTAAAAATAAAAAAATAGCTGGGCGTGGTGGTGG	13876
Db	13561	ACAGGTGAATCCCGTCTCTACTAAAAATAAAAAAATAGCTGGGCGTGGTGGTGG	13620
QY	13877	TGCCTGTAGTCCCAAGTACTCAGGAGGCTGAGGCAGGAGAAATGGCATGAACCTGGGAGGT	13936
Db	13621	TGCCTGTAGTCCCAAGTACTCAGGAGGCTGAGGCAGGAGAAATGGCATGAACCTGGGAGGT	13680
QY	13937	GGAGTTGCAATGAGCCGAGATCTGTCGCACTACGCTGGGTGACAGAGCCAGAC	13996
Db	13681	GGAGTTGCAATGAGCCGAGATCTGTCGCACTGTCGCACTGAGCCCTGGGTGACAGAGCCAGAC	13740
QY	13997	TCTATCTCAGAAAAAATAAAAAAAGAGAGAAATGGGCTCTGCAAGGAGACAAGGGTACCAGC	14056
Db	13741	TCTATCTCAGAAAAAATAAAAAAAGAGAGAAATGGGCTCTGCAAGGAGACAAGGGTACCAGC	13800
QY	14057	GGGAGGACATTTGAGCCAAAGAGGTAGAGTCTTTTGATGATCAGCAGGAGTATCTCTCC	14116
Db	13801	GGGAGGACATTTGAGCCAAAGAGGTAGAGTCTTTTGATGATCAGCAGGAGTATCTCTCC	13860
QY	14117	GTAACAAACCCAAAGAAACCCAGAGGGCAGATGGTGGGCAAGAGCCCTAGAGGCAAGGAGTG	14176
Db	13861	GTAACAAACCCAAAGAAACCCAGAGGGCAGATGGTGGGCAAGAGCCCTAGAGGCAAGGAGTG	13920

QY	14177	TAGGTTGGTGTGTGCTCTGTGTGGCTCACAGCACTCTCCACAGATTCACAGGACCA	14236
Db	13921	TAGGTTGGTGTGTGCTGTGTGGCTCACAGCACTCTCCACAGATTCACAGGACCA	13980
QY	14237	CTTAATATTACCAATGAACACCAACTCTGTGCGCAAGCCCTGAGCTAGGTAGCGGGCTAAC	14296
Db	13981	CTTAATATTACCAATGAACACCAACTCTGTGCGCAAGCCCTGAGCTAGGTAGCGGGCTAAC	14040
QY	14297	AACACAGCAAAACAGAACAGCCCTGATTTATTATTATTATTATTATTATTATTATTATT	14356
Db	14041	AACACAGCAAAACAGAACAGCCCTGATTTATTATTATTATTATTATTATTATTATTATT	14100
QY	14357	TATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT	14416
Db	14101	TATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT	14160
QY	14417	TGCAGTGGAGGATCTCAGCTCACTGCAACCTCTGCCCTCCCGGGTTCAAGCGATTCTCCT	14476
Db	14161	TGCAGTGGAGGATCTCAGCTCACTGCAACCTCTGCCCTCCCGGGTTCAAGCGATTCTCCT	14220
QY	14477	GCCTTGGCTCCCAAGTAGCTGGGACTACAGGCATGTGCCACCATGTCTACTATTATTTT	14536
Db	14221	GCCTTGGCTCCCAAGTAGCTGGGACTACAGGCATGTGCCACCATGTCTACTATTATTTT	14280
QY	14537	ATATTGCTAGTAGAGTAGGGCTTCGCCCATGTGSCCAGGCTGTGTTTGAACCTCTGACC	14596
Db	14281	ATATTGCTAGTAGAGTAGGGCTTCGCCCATGTGSCCAGGCTGTGTTTGAACCTCTGACC	14340
QY	14597	TCAGTGATCTGCCACCTCGGCTCCCAAAAGTGTGGGATTACAGGCATGAGCACCGC	14656
Db	14341	TCAGTGATCTGCCACCTCGGCTCCCAAAAGTGTGGGATTACAGGCATGAGCACCGC	14400
QY	14657	ACCAGCCCTCAACAAATATTATTATTAGTCTCAATGAGTAGGACAGTGTACTGTCTT	14716
Db	14401	ACCAGCCCTCAACAAATATTATTATTAGTCTCAATGAGTAGGACAGTGTACTGTCTT	14460
QY	14717	AGCGAAACAAACAGACCCCTGCCCTTAGGGAGCTCACAGGAGAAAGCAGATAGTACACA	14776
Db	14461	AGCGAAACAAACAGACCCCTGCCCTTAGGGAGCTCACAGGAGAAAGCAGATAGTACACA	14520
QY	14777	GATAGATGTAAATTAATAAGTAATAAGTGCAGGAAGTCTGTCCATGGTGAACCAAGG	14836
Db	14521	GATAGATGTAAATTAATAAGTAATAAGTGCAGGAAGTCTGTCCATGGTGAACCAAGG	14580
QY	14837	GGTGGTAAGAGAGGATCTGACCCAGTTTAAAGTCAAGGCGAGCCCTCTATGAGTGAT	14896
Db	14581	GGTGGTAAGAGAGGATCTGACCCAGTTTAAAGTCAAGGCGAGCCCTCTATGAGTGAT	14640
QY	14897	GCTTGAGTCAAGGTCTAAAGGTGTTTGGGAGACAACCTAGGAGGAAGGGAGGGAGAG	14956
Db	14641	GCTTGAGTCAAGGTCTAAAGGTGTTTGGGAGACAACCTAGGAGGAAGGGAGGGAGAG	14700
QY	14957	CTTTACAGGAAGACCTAACCGCACATCCAGAGCCCTGAGGTGGAGGGAGGACAATGAG	15016
Db	14701	CTTTACAGGAAGACCTAACCGCACATCCAGAGCCCTGAGGTGGAGGGAGGACAATGAG	14760
QY	15017	TGTCAAGCCAGGCTGGTGGACCATAGGACCTGGGAGAGACAACCTGCACTGTC	15076
Db	14761	TGTCAAGCCAGGCTGGTGGACCATAGGACCTGGGAGAGACAACCTGCACTGTC	14820
QY	15077	AGTCTCAGCCCTGCTCAGTCAATGAGTCAATGGAATAAATCTTAAACAGAGGGAGGATTA	15136
Db	14821	AGTCTCAGCCCTGGCTCTCAGTCAATGAGTCAATGGAATAAATCTTAAACAGAGGGAGGATTA	14880
QY	15137	AAGGGTTTACAAAGCATAGGGAGACATGACCTGGTTTATTATTATTATTATTATTATT	15196
Db	14881	AAGGGTTTACAAAGCATAGGGAGACATGACCTGGTTTATTATTATTATTATTATTATT	14940
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Db	14941	TGCCTGCTAGTAGAGATGCAATTAGAAAGGGAGCCGTCCATGTAGAGGAGCAAGTGTG	15000

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Db	15001	GAAGCTGTGACAGCAGCTTAGTCTTGGGCCCCCTCCTCGGGGGCCGAGCAGGAAAAAGG	15060
QY	15317	TAGAGAAGGACCCCTAGCTGAAAGCCAGGTGTCTCCCTGGAGTGGCAGACCCATGTCA	15376
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QY	15377	CCAGAGAGCTTTTACACATAACGATTTCTCAGGTCCACACCCCGAGATTTATAGAGTTAGAA	15436
Db	15121	CCAGAGAGCTTTTACACATAACGATTTCTCAGGTCCACACCCCGAGATTTATAGAGTTAGAA	15180
QY	15437	AATCTGSCAGTGGGACCCAGCAATCTGTTTACCACCCCTCTAGGGAATTCGGCTTAG	15496
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Db	15241	AGGCTAAGAACCAACAGATTTCTAGAGCTGCACTGCTTGGGTTTCATTTCTGGCTCTGTCC	15300
QY	15557	TTTACCTGCTGTGCTGCTTGGGCAAGTTACTTTAAAGTCTCTGTGTAGTCTCTCTCTCT	15616
Db	15301	TTTACCTGCTGTGCTGCTTGGGCAAGTTACTTTAAAGTCTCTGTGTAGTCTCTCTCTCT	15360
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Db	15361	GTAAATGGAAACGATAGCAGGCTTTTCTGGAAACAGCATATGATAAGCTATCTTAAAAA	15420
QY	15677	AAAAAGAAAGAAAGAGCTAAGTGTGTTTGTGTAATAATAATAAACCTCCAGGCTAT	15736
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QY	15737	GGGAGTTCAGAGAAATTAAGCCAAAGCAGAGGTAGGAGGTGGCCATTTTCTCTCTCT	15796
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Db	15541	AGCGATTCTCATCT	15600
QY	15857	TGTGTAAGTCTTAACCT	15916
Db	15601	TGTGTAAGTCTTAACCT	15660
QY	15917	GCCT	15976
Db	15661	GCCT	15720
QY	15977	TCTTCGGGGCGAGTCCAGGACGCTGCAATCTCCGACTTCAGCTTCTCTCTCTCTCTCT	16036
Db	15721	TCTTCGGGGCGAGTCCAGGACGCTGCAATCTCCGACTTCAGCTTCTCTCTCTCTCTCT	15780
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DB	23221	CTGGGTCT	23280
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QY	23597	TCCCT	23656
DB	23341	TCCCT	23400
QY	23657	CTGTCT	23716
DB	23401	CTGTCT	23460
QY	23717	CCCTTTCT	23776
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QY	23777	TGTTCTGTCT	23836
DB	23521	TGTTCTGTCT	23580
QY	23837	CATGTAATCT	23896
DB	23581	CATGTAATCT	23640
QY	23897	GTCT	23956
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QY	23957	TCTCTGTCT	24016
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QY	24017	CCT	24076
DB	23761	CCT	23820
QY	24077	CT	24136
DB	23821	CT	23880
QY	24137	TCTCGGATCTCATGCT	24196
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QY	24197	CTCTGGGTCTACCTGTCTCGGCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	24256
DB	23941	CTCTGGGTCTACCTGTCTCGGCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	24000
QY	24257	CACAGTTCTCTGACCAAGACCCAGGGAAGCCCTGGGCTCAGGGCTCAGGGGAACCTTA	24316
DB	24001	CACAGTTCTCTGACCAAGACCCAGGGAAGCCCTGGGCTCAGGGCTCAGGGGAACCTTA	24060
QY	24317	CCATCCGTGACATGGCTTTTTCGCTGGATTGACTGGGAGCGCTGGAAACGATTGGAGA	24376
DB	24061	CCATCCGTGACATGGCTTTTTCGCTGGATTGACTGGGAGCGCTGGAAACGATTGGAGA	24120
QY	24377	TCCCGCTCTCTTTCAGACCCCGCCCGGTCTAGTCACTCTCTCTCTCTCTCTCTCTCTCTCT	24436
DB	24121	TCCCGCTCTCTTTCAGACCCCGCCCGGTCTAGTCACTCTCTCTCTCTCTCTCTCTCTCTCT	24180
QY	24437	CTGAAGGGGTGGGTTCCTCTGGGCTCAATATACCTGTATGTGGGGTGGGGTTCCTCTC	24496
DB	24181	CTGAAGGGGTGGGTTCCTCTGGGCTCAATATACCTGTATGTGGGGTGGGGTTCCTCTC	24240
QY	24497	TGCAGAGCCCCCGCCCAACAAAGGAGGTGCAGACACCATGAAGCATGAATAGAGAT	24556
DB	24241	TGCAGAGCCCCCGCCCAACAAAGGAGGTGCAGACACCATGAAGCATGAATAGAGAT	24300
QY	24557	TCTGCAGAGACAGAGATGAGACTGGGGTACAGAGGGACACCCGAGGAGCCCTCGA	24616
DB	24301	TCTGCAGAGACAGAGATGAGACTGGGGTACAGAGGGACACCCGAGGAGCCCTCGA	24360
QY	24617	GCTGCTTAACCTTCCCTCTCCCGACCTCTCCACAGTGTGGCGGAGCGGCGGAGAACTT	24676
DB	24361	GCTGCTTAACCTTCCCTCTCCCGACCTCTCCACAGTGTGGCGGAGCGGCGGAGAACTT	24420
QY	24677	ACAAAGTTCTTTCAGCGGGCGGCGGCGGCTGACCCCTTCCAGACCGCTAGTCTTGCCA	24736
DB	24421	ACAAAGTTCTTTCAGCGGGCGGCGGCGGCTGACCCCTTCCAGACCGCTAGTCTTGCCA	24480
QY	24737	GCATCGACAGGCGGATTTCCAGGGCTTCACTAGTGAAACCCCGACTTCGTGCAACCGG	24796
DB	24481	GCATCGACAGGCGGATTTCCAGGGCTTCACTAGTGAAACCCCGACTTCGTGCAACCGG	24540
QY	24797	ATGCCCGAGGCGGCGGCGGCGGCGGCTGACCCCTTCCAGACCGCTAGTCTTGCCA	24856
DB	24541	ATGCCCGAGGCGGCGGCGGCGGCGGCTGACCCCTTCCAGACCGCTAGTCTTGCCA	24600
QY	24857	TAGGTGTCTCCAAAGCTCTCCCGCTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCT	24916
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QY	24917	ACCAACCCCTGTGCGATTTCTAGATCTCTGACCCAGGATTCAGCTCTGCGCGCGGGT	24976
DB	24661	ACCAACCCCTGTGCGATTTCTAGATCTCTGACCCAGGATTCAGCTCTGCGCGCGGGT	24720
QY	24977	TCTAGACGCGGCTTCCAGAGCGTCTCTGGCTTCTGAACTCATACAGCTCTTACAGCGGT	25036
DB	24721	TCTAGACGCGGCTTCCAGAGCGTCTCTGGCTTCTGAACTCATACAGCTCTTACAGCGGT	24780
QY	25037	CCCGGCTTCAAGACTTGAGCG 25057	
DB	24781	CCCGGCTTCAAGACTTGAGCG 24801	







GenCore version 5.1.9  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
 OM nucleic - nucleic search, using sw model  
 Run on: October 20, 2006, 09:25:04 ; Search time 506 Seconds  
 (without alignments)  
 2.881 Million cell updates/sec

Title: US-10-671-007-3  
 Perfect score: 25301  
 Sequence: 1 agccccggaggggtgtg.....tagttctagatgagtgagg 25301

Scoring table: IDENTITY\_NUC  
 Gap 10.0 , Gapext 0.5  
 Searched: 1 seqs, 28806 residues

Total number of hits satisfying chosen parameters: 2  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries  
 Database : US6812339-13217:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25233.4	99.7	28806	1	US-09-949-016-13217, A
2	576.397	2.3	28806	1	US-09-949-016-13217, A

# ALIGNMENTS

RESULT 1  
 US-09-949-016-13217  
 ; Sequence 13217, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; PRIOR FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13217  
 ; LENGTH: 28806  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-13217  
 Query Match 99.7% ; Score 25233.4 ; DB 1 ; Length 28806 ;

Best Local Similarity 99.9% ; Pred. No. 0 ; Matches 25284 ; Conservative 0 ; Mismatches 6 ; Indels 14 ; Gaps 4 ;									
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QY	61	TCTCCGGAGGGAGCGCTTTAAGCCGAAACCCGCCCTCTCGGTCTCTCGCAACGC	120						
DB	1817	TCTCCGGAGGGAGCGCTTTAAGCCGAAACCCGCCCTCTCGGTCTCTCGCAACGC	1876						
QY	121	CTCCCCCAACCCGGGGTCTCCACATTTTCAGCAGGTGCGGAGCTGGAGCTCCACCGCG	180						
DB	1877	CTCCCCCAACCCGGGGTCTCCACATTTTCAGCAGGTGCGGAGCTGGAGCTCCACCGCG	1936						
QY	181	CGGCCGCTGCTCCGGTCCCGGCGCCCTCTTGGCTCTTCTCCCTCCCACTCCCGCCG	240						
DB	1937	CGGCCGCTGCTCCGGTCCCGGCGCCCTCTTGGCTCTTCTCCCTCCCACTCCCGCCG	1996						
QY	241	TCCCTCTGGGAGCGCGCGCGCGCGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC	300						
DB	1997	TCCCTCTGGGAGCGCGCGCGCGCGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC	2056						
QY	301	GGAGGTGCTTGGCCCTCTCTGCCCCACCTCGGAATTTCCCTGTGGTCTCTTGTATCCT	360						
DB	2057	GGAGGTGCTTGGCCCTCTCTGCCCCACCTCGGAATTTCCCTGTGGTCTCTTGTATCCT	2116						
QY	361	CGAGTCTCCAGCTCTCTCCCTTCCACCTGTTTCCCAAGAAAGGAGGATCTGTGTC	420						
DB	2117	CGAGTCTCCAGCTCTCTCCCTTCCACCTGTTTCCCAAGAAAGGAGGATCTGTGTC	2176						
QY	421	CTGTCTAGTTTCTGGGCGCATGGCTGTGTGGGCGCGCGCTAGCGATTTCAGAGGGGG	480						
DB	2177	CTGTCTAGTTTCTGGGCGCATGGCTGTGTGGGCGCGCGCTAGCGATTTCAGAGGGGG	2236						
QY	481	ACCCCGCCCTGTTTTCAGAAAGGGGGCCCTGAGGCAGAAAGTGTGTCTCAAGTCAA	540						
DB	2237	ACCCCGCCCTGTTTTCAGAAAGGGGGCCCTGAGGCAGAAAGTGTGTCTCAAGTCAA	2296						
QY	541	GAGCCACAGTTTACCGCTGCTTCTTCAAGCAGCCACCTTCTGCAGCCACTGCACCGA	600						
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QY	601	CTTCATCTGTGTAGGGAAGGGGGCTGGGGGACGAGGGGACTAGGGGTGCAGA	660						
DB	2357	CTTCATCTGTGTAGGGAAGGGGGCTGGGGGACGAGGGGACTAGGGGTGCAGA	2416						
QY	661	CTCCTATCACGCCGACCCCTGTGGAAGAAAGAGGGGGCTGTAGTCCCGACTCCAG	720						
DB	2417	CTCCTATCACGCCGACCCCTGTGGAAGAAAGAGGGGGCTGTAGTCCCGACTCCAG	2476						
QY	721	GTTCTAGGATGGCCAGGAAAGCTGGGAGCTTTCAGCTCTGGGTTTCAGTGAGGAGG	780						
DB	2477	GTTCTAGGATGGCCAGGAAAGCTGGGAGCTTTCAGCTCTGGGTTTCAGTGAGGAGG	2536						
QY	781	CTGGTCTCTGAGTGTGGGTCCGAGGAGGAGGAGCTCGAGGACAGAGGCTCTGAGT	840						
DB	2537	CTGGTCTCTGAGTGTGGGTCCGAGGAGGAGGAGGCTCGAGGACAGAGGCTCTGAGT	2596						
QY	841	CTTGGGTCTGAGGAGGAAAGGGCTTGGGGGGCTGGGAGCTTGGATTCTTGGGTCTGA	900						
DB	2597	CTTGGGTCTGAGGAGGAAAGGGCTTGGGGGGCTGGGAGCTTGGATTCTTGGGTCTGA	2656						
QY	901	AGGAAGAACTGGGGGCTGAACTCCAGTCTAAGGAAGAGGGCTGGGGGCCAAATTC	960						
DB	2657	AGGAAGAACTGGGGGCTGAACTCCAGTCTAAGGAAGAGGGCTGGGGGCCAAATTC	2716						
QY	961	TGGGTCTTAGAAAGAGGAGGTGGCCGGGCTTGACACCTGGGGCCCTGGGAGAGGGT	1020						
DB	2717	TGGGTCTTAGAAAGAGGAGGTGGCCGGGCTTGACACCTGGGGCCCTGGGAGAGGGT	2776						
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Db 2837 CTGACCTAGGATCCCTGACTTCTCAGGGGTATCGGAAAGCAGGCGCTGCAATGTCAAGG 2896  
Qy 1141 TAAAGCTGTGGGACCGGGGCTCTGGGACCTCAGGAGGTTGGAGGCTGGGGCCCAACAG 1200  
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Qy 1381 AATCTGTGGCATGGGAACATGGAGATTTGGAAAAGGGGAGCTCAAGGGGGGGAAGGGGA 1440  
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Qy 1501 CACAGCCGTCCTAGGACAGGGGAGGCGCGGTGGGGTCAACAATGGGCGAGTGGGGGCGG 1560  
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Qy 1681 ACTTCTGCCCAAGTGTGCTTCTCGGGCTGCGTCTGAAGATATTTTCGGTTTTCGCTCTT 1740  
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Db 3497 TGAATCTGTCTGCTCTCTCTGCTGCTTGTGATCTCGTGGGCGCTGTGTCTGTTG 3556  
Qy 1801 TCAATGGGATCTATTTTCTTCTCTCTTTTCCATCTCCCTTCCCTGAGCTCTGTGCTC 1860  
Db 3557 TCAATGGGATCTATTTTCTTCTCTCTTTTCCATCTCCCTTCCCTGAGCTCTGTGCTC 3616  
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Db 3617 TGTGTCTCTGTGAAGTCTCTGCGTCTCTGTTCTGACTCTGAGCCCATCTCTTGGGTTT 3676  
Qy 1921 CTGTCTCTGCTCTCTCTCTGCGCTCCGATTTTCTCTGTGTGGAGCTCTGTGTGTGAG 1980  
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Qy 2281 GCTGGAGGGGAGGGGGGCTGGAGAGATAGGGGGAGCTATCTGGGCCAGATTTCTTGCCC 2340  
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Db 7509 TGAGACTCCATCTCAAAAAAAAAAAAAAAAAAGTAAATGATGATCAAGATTGGCNA 7568  
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Db 7569 AATGATTTCATTAGTCCCAAGGAGGACATGCCCCCACTTTCAAGCGGTAAATCTG 7628  
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Qy 6301 AACAAAGCAGATATTTGCTCCGGGGTATGTTGGTGGCAGGGAGAGGAGTCTCACTGA 6360  
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Qy 6361 TGACCTGCATTTCTGCTTAATGACTCTGAAATTTAGCATTTGCTTCAAAATATAGATTA 6420  
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Qy 6541 AATAAAATCCCTAAACAATAACACAGTAATAGTATTGGAGGATCTAAAGTGGTAGGCAC 6600  
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Qy 6781 TGGGAGTTGGGGGATGGGAACATATGGGAGGTTGGAAGCTCTCTCTCTCTCTCTCTCTG 6840  
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Db 8949 GACCACTGTTTAAATTTCAATCCCCCACTTCTGGTGGTCCCATCCCTGCTCATTT 9008  
Qy 7261 TTTTCTCCAGAGCACCCATTAACCAACCATCAACATATATGTTTATTTTACCATGTT 7320  
Db 9009 TTTTCTCCAGAGCACCCATTAACCAACCATCAACATATATGTTTATTTTACCATGTT 9068  
Qy 7321 TACATTTCTGATTCCTTCCATTTAGGAAGTAACTCCATGTGACAAAGAGGTTTTTTTTT 7380  
Db 9069 TACATTTCTGATTCCTTCCATTTAGGAAGTAACTCCATGTGACAAAGAGGTTTTTTTTT 9128  
Qy 7381 CATTTGTTTATGCTGGGTTCCCAACCAAGAAAGTCCCTGGCACACAGAGGTTCTCA 7440  
Db 9129 CATTTGTTTATGCTGGGTTCCCAACCAAGAAAGTCCCTGGCACACAGAGGTTCTCA 9188  
Qy 7441 ATGATTATTTGGTACATAGATGAAAGAGATGGAGCTCAGGCTGACCTAGAGAGCAAGGC 7500  
Db 9189 ATGATTATTTGGTACATAGATGAAAGAGATGGAGCTCAGGCTGACCTAGAGAGCAAGGC 9248  
Qy 7501 AGGAGGAAAAGATAAAGGGCCCCCTCCCTGGGGTTTTAGGACCTTCCCAAGCCCCCTTA 7560  
Db 9249 AGGAGGAAAAGATAAAGGGCCCCCTCCCTGGGGTTTTAGGACCTTCCCAAGCCCCCTTA 9308  
Qy 7561 AGCCAGTCTTCTCTGCCCCCAGGACCCCGGAAACAAACACAGATTTCCGCTCATAGCTTA 7620  
Db 9309 AGCCAGTCTTCTCTGCCCCCAGGACCCCGGAAACAAACACAGATTTCCGCTCATAGCTTA 9368





D	b	11529	TCTGGGGTCAGGGAGGGAATGACAGCTCAGACAGATGATCTGAGGCTCTAGTGGCC	11588
Q	y	9841	CCAGAGAGCAGCTGATGGAGGGTTPAGATAGAGGAAACCCAGAAAGGGCAGAGAA	9900
D	b	11589	CCAGAGAGCAGCTGATGGAGGGTTPAGATAGAGGAAACCCAGAAAGGGCAGAGAA	11648
Q	y	9901	GATGGTGGGAAAGGGAATAGATGATTGAGGAGTGGGATGAGATACAGAAACGGAGA	9960
D	b	11649	GATGGTGGGAAAGGGAATAGATGATTGAGGAGTGGGATGAGATACAGAAACGGAGA	11708
Q	y	9961	GACAGCCAGACCACTGTATATATAGTCTCCATTTGAAGCCCCCAACTTTAGAGTTAGACAG	10020
D	b	11709	GACAGCCAGACCACTGTATATATAGTCTCCATTTGAAGCCCCCAACTTTAGAGTTAGACAG	11768
Q	y	10021	AGATGAGAGAGAGAGAGAGTCTCAGAAAGAGCGCAGAAACCCAAAGAGAGACACAGATG	10080
D	b	11769	AGATGAGAGAGAGAGAGAGTCTCAGAAAGAGCGCAGAAACCCAAAGAGAGACACAGATG	11828
Q	y	10081	GAGAGGGGGGAGAGATGGGGATGGCAGGAGAGACAGAGATCAGTTGACAGGAGAGACA	10140
D	b	11829	GAGAGGGGGGAGAGATGGGGATGGCAGGAGAGACAGAGATCAGTTGACAGGAGAGACA	11888
Q	y	10141	GAGTGTAGAGACCCAGAGAGGAGAGAGGCTACAGAGACTCAGAGAGAGAGATCTCGAG	10200
D	b	11889	GAGTGTAGAGACCCAGAGAGGAGAGAGGCTACAGAGACTCAGAGAGAGAGATCTCGAG	11948
Q	y	10201	AGACAAGAGACAGAGATGGGAAGGGCGGAGAAATGCAAGGAGGAGGAGGAGAGCTC	10260
D	b	11949	AGACAAGAGACAGAGATGGGAAGGGCGGAGAAATGCAAGGAGGAGGAGGAGAGCTC	12008
Q	y	10261	TCTAGTTTACTTCAGGCCCCAAGCCCTAGCTGGAGAGAGAGCCGGCTGGGAAGGTCA	10320
D	b	12009	TCTAGTTTACTTCAGGCCCCAAGCCCTAGCTGGAGAGAGAGCCGGCTGGGAAGGTCA	12068
Q	y	10321	GAGTCTGAGACCGACAAAGCAGAGAGAGGAGCCAGCTGGCTGGGTTTCCGCCCACTC	10380
D	b	12069	GAGTCTGAGACCGACAAAGCAGAGAGAGGAGCCAGCTGGCTGGGTTTCCGCCCACTC	12128
Q	y	10381	CAGCAACAAGATGGGAAACCGAGGGAGGCCATGAGCTCGGCTCTGACCCCATCCACCC	10440
D	b	12129	CAGCAACAAGATGGGAAACCGAGGGAGGCCATGAGCTCGGCTCTGACCCCATCCACCC	12188
Q	y	10441	CACCTTCTCAGCAACCTCAGCCAGGGGATGTGGAGCGCCGGCTCAGCGTGGAGGTGT	10500
D	b	12189	CACCTTCTCAGCAACCTCAGCCAGGGGATGTGGAGCGCCGGCTCAGCGTGGAGGTGT	12248
Q	y	10501	GGGACTGGGACCGGACCTCCCGCAACGACCTTCATGGGGGCGCATGTCTTTGGCGTCTCGG	10560
D	b	12249	GGGACTGGGACCGGACCTCCCGCAACGACCTTCATGGGGGCGCATGTCTTTGGCGTCTCGG	12308
Q	y	10561	AGCTGTCAAAGGCGCCGCTGGATGGCTGGTGGAGCAGGGCTGGGGCTGGGGATGGAG	10620
D	b	12309	AGCTGTCAAAGGCGCCGCTGGATGGCTGGTGGAGCAGGGCTGGGGCTGGGGATGGAG	12368
Q	y	10621	CGCAATATACCACTCCCATCTGTGTGTGTCTCTCTCTCCAGGCGCACCTGTCTTCCCT	10680
D	b	12369	CGCAATATACCACTCCCATCTGTGTGTGTCTCTCTCTCCAGGCGCACCTGTCTTCCCT	12428
Q	y	10681	CTGCGCTCCAGCATGGGCACACACACACACACACACACACACACACACACACACAC	10740
D	b	12429	CTGCGCTCCAGCATGGGCACACACACACACACACACACACACACACACACACACAC	12488
Q	y	10741	ACAGCCCT	10800
D	b	12489	ACAGCCCT	12548
Q	y	10801	TTTATCTCACTTTCT	10860
D	b	12549	TTTATCTCACTTTCT	12608
Q	y	10861	TTCCAAATGTCTTGGCTCTCCCATGGGTGCCCATCCCGCTCCCGCTCTGGTCTCCG	10920
D	b	12609	TTCCAAATGTCTTGGCTCTCCCATGGGTGCCCATCCCGCTCCCGCTCTGGTCTCCG	12668

Q	y	10921	TCTGTATGTCAAGTACTGAAACCCAGAGAGGGCGAGTATTACAATGTGCCGT	10980
D	b	12669	TCTGTATGTCAAGTACTGAAACCCAGAGAGGGCGAGTATTACAATGTGCCGT	12728
Q	y	10981	GGCCCATGCTGACAACTGCAGGCTCTCCAGAAAGTTTGAGGTACCCAGACCCCTGGCTTC	11040
D	b	12729	GGCCCATGCTGACAACTGCAGGCTCTCCAGAAAGTTTGAGGTACCCAGACCCCTGGCTTC	12788
Q	y	11041	TCAGGGAGCCAGCCCAAGCTCCCAAGTTCAGAGCTGGCCCTTCTCTTCCACCCCTGAG	11100
D	b	12789	TCAGGGAGCCAGCCCAAGCTCCCAAGTTCAGAGCTGGCCCTTCTCTTCCACCCCTGAG	12848
Q	y	11101	TGCCCGCTGGTCTCTGGGACTACAGTTCCAGAGAGCCCTAGGACTCCCTCTCTCTCTCT	11160
D	b	12849	TGCCCGCTGGTCTCTGGGACTACAGTTCCAGAGAGCCCTAGGACTCCCTCTCTCTCTCT	12908
Q	y	11161	CTAGGGGACTCAGAGCCCAAGGCTCTGATGGGAATTTATAGTTCTCTATCTATCTGCTT	11220
D	b	12909	CTAGGGGACTCAGAGCCCAAGGCTCTGATGGGAATTTATAGTTCTCTATCTATCTGCTT	12968
Q	y	11221	TCAGGGTACTAGGGGCAACAGCCCTCTGTTCTAGGGCGATCCCTCTGCTCTCTTGGGACC	11280
D	b	12969	TCAGGGTACTAGGGGCAACAGCCCTCTGTTCTAGGGCGATCCCTCTGCTCTCTTGGGACC	13028
Q	y	11281	CTGACT	11340
D	b	13029	CTGACT	13088
Q	y	11341	GTAGAAACAGGGCGTTGAATGGAGCAGTTTGTGCTACTTCTCTGATTTCTTATCTCTC	11400
D	b	13089	GTAGAAACAGGGCGTTGAATGGAGCAGTTTGTGCTACTTCTCTGATTTCTTATCTCTC	13148
Q	y	11401	CTCTGACT	11460
D	b	13149	CTCTGACT	13208
Q	y	11461	TCCTGTCTGTCTGAATTAATCCAGGATCCAGAGATGAATCTCACCTCAAGCAACTCTCC	11520
D	b	13209	TCCTGTCTGTCTGAATTAATCCAGGATCCAGAGATGAATCTCACCTCAAGCAACTCTCC	13268
Q	y	11521	AAAGTAGGGACACAGTCAAGATCTTAAATACAGGAAGATGTGCTAAATTAGAGGTAG	11580
D	b	13269	AAAGTAGGGACACAGTCAAGATCTTAAATACAGGAAGATGTGCTAAATTAGAGGTAG	13328
Q	y	11581	CCAGGGCACTCAAGAGCCCTAACCGAGCCTAATCCAGCCTGGGGAGGGTGGTCAAG	11640
D	b	13329	CCAGGGCACTCAAGAGCCCTAACCGAGCCTAATCCAGCCTGGGGAGGGTGGTCAAG	13388
Q	y	11641	GAGGACTTCCCTGAGGAGTACGCTGAATTTGATTTCTTGAGGTTTTTAAATTTTTTTA	11700
D	b	13389	GAGGACTTCCCTGAGGAGTACGCTGAATTTGATTTCTTGAGGTTTTTAAATTTTTTTA	13448
Q	y	11701	ATTTATTTTTTATTTTTTATTTTTTATTTTTTATTTTTTATTTTTTATTTTTTATTTTT	11760
D	b	13449	ATTTATTTTTTATTTTTTATTTTTTATTTTTTATTTTTTATTTTTTATTTTTTATTTTT	13508
Q	y	11761	GAATCTCGCTCAGTCAACCTCCAGCTCCCGGTTCAAGCAATTTCTTGCTCTCAGCCT	11820
D	b	13509	GAATCTCGCTCAGTCAACCTCCAGCTCCCGGTTCAAGCAATTTCTTGCTCTCAGCCT	13568
Q	y	11821	CTGAGTAGTGGGATTTACAGGTGACCGCCACACACACACACACACACACACACACAC	11880
D	b	13569	CTGAGTAGTGGGATTTACAGGTGACCGCCACACACACACACACACACACACACACAC	13628
Q	y	11881	TAGTAGAGATGGGATTTGCCCATGTTGGCAGGCTGATCTCAAACTCCCAAACTCAGGTG	11940
D	b	13629	TAGTAGAGATGGGATTTGCCCATGTTGGCAGGCTGATCTCAAACTCCCAAACTCAGGTG	13688
Q	y	11941	ATCCGCTGCTTGGCTTCCCAAGGCTGGGATTTACAGGATGAGCCACTGCGGCCGAC	12000
D	b	13689	ATCCGCTGCTTGGCTTCCCAAGGCTGGGATTTACAGGATGAGCCACTGCGGCCGAC	13748





QY	16381	ATAGGTGATGCTGGCCGAGCGAGGGGCTCTGATGAGCTCTAGCCCATCAAGATCTTGAA	16440
Db	18126	ATAGGTGATGCTGGCCGAGCGAGGGGCTCTGATGAGCTCTAGCCCATCAAGATCTTGAA	18185
QY	16441	AAAGGACGTGATCGTCCAGGACGACGATGTGGACTGCAACGCTGGTGAGAAAAGTGTGCT	16500
Db	18186	AAAGGACGTGATCGTCCAGGACGACGATGTGGACTGCAACGCTGGTGAGAAAAGTGTGCT	18245
QY	16501	GGCGCTGGGGGGCGGGGCTCTGGCGCGCGGCCCTCTCTCCTCACCAGCTCCACTCCAC	16560
Db	18246	GGCGCTGGGGGGCGGGGCTCTGGCGCGCGGCCCTCTCTCCTCACCAGCTCCACTCCAC	18305
QY	16561	CTTCCAGACCCCGGTAAAGATGAGGGGGGCGAGGCTGTCTCTCGGGGCCCTGCTTTATCC	16620
Db	18306	CTTCCAGACCCCGGTAAAGATGAGGGGGGCGAGGCTGTCTCTCGGGGCCCTGCTTTATCC	18365
QY	16621	AGTTCTGGACATCTGCGTTGGGATTTCTGAGTTTAGGGCGAGGCAAGAGAACTTTGTGCTC	16680
Db	18366	AGTTCTGGACATCTGCGTTGGGATTTCTGAGTTTAGGGCGAGGCAAGAGAACTTTGTGCTC	18425
QY	16681	TCTGAGTGGGCGAGGCGAGCGGATTTCTCTCCTCAGGGGCGTGCGC-GGGGGGGGGTCC	16739
Db	18426	TCTGAGTGGGCGAGGCGAGCGGATTTCTCTCCTCAGGGGCGTGCGC-GGGGGGGGGTCC	18485
QY	16740	TTGGGGGGCGTGCCAGCGAAGGGACTCATCGGGGGCGTGCGCCAGCGGAGGGGCTCA	16799
Db	18486	TTGGGGGGCGTGCCAGCGAAGGGACTCATCGGGGGCGTGCGCCAGCGGAGGGGCTCA	18545
QY	16800	ACGGAGCGAGGCGGGGTGAGGGGCTCTCTCGGGGGCGTGCGCCAGGTGAGGGGACTCATC	16859
Db	18546	ACGGAGCGAGGCGGGGTGAGGGGCTCTCTCGGGGGCGTGCGCCAGGTGAGGGGACTCATC	18605
QY	16860	GGGGGGCGTGCCAGGCGAGAGGGGCTCTTCGCGGGGCGTGCTCAGGCGGATGAAATCTTTG	16919
Db	18606	GGGGGGCGTGCCAGGCGAGAGGGGCTCTTCGCGGGGCGTGCTCAGGCGGATGAAATCTTTG	18665
QY	16920	GGGGGGGTGTTTAGAGGGGCGGGCTTTTGTGAGCGGATGGGATCATTAATAGGCGTGCCCA	16979
Db	18666	GGGGGGGTGTTTAGAGGGGCGGGCTTTTGTGAGCGGATGGGATCATTAATAGGCGTGCCCA	18725
QY	16980	GGCAGATTGGCTCTTTGGGGGCGAGGCGAGGACGAGAGATTAATGATGAGCGTATCCAG	17039
Db	18726	GGCAGATTGGCTCTTTGGGGGCGAGGCGAGGACGAGAGATTAATGATGAGCGTATCCAG	18785
QY	17040	GCAAGTATGATTTCTCGAGGGCGGTGTGCGGGCGGATGAGTCTCTCGGGGCGGTGGCCAGG	17099
Db	18786	GCAAGTATGATTTCTCGAGGGCGGTGTGCGGGCGGATGAGTCTCTCGGGGCGGTGGCCAGG	18845
QY	17100	CGGTGAGTTCTCTCGGTGGCATGGCCTGGCCAGGTGAATGGGTCTCTCGGAGGTGTCTGTA	17159
Db	18846	CGGTGAGTTCTCTCGGTGGCATGGCCTGGCCAGGTGAATGGGTCTCTCGGAGGTGTCTGTA	18905
QY	17160	AGCGGTTGAGTTCTTTGGGGGCGTGCGAGGTGGATGGGCTCTTTGGGGGGGAGTGGCCAGA	17219
Db	18906	AGCGGTTGAGTTCTTTGGGGGCGTGCGAGGTGGATGGGCTCTTTGGGGGGGAGTGGCCAGA	18965
QY	17220	TGCTCTGTTCCCTGGGGAGCTTGGTCTTGAGTGGCTGTAGCCAGTGTCTCTGGAATTTTCA	17279
Db	18966	TGCTCTGTTCCCTGGGGAGCTTGGTCTTGAGTGGCTGTAGCCAGTGTCTCTGGAATTTTCA	19025
QY	17280	GCAAGGGGCGACAGTGGAGGGGCTCTCTCTAGTGGGCTCTGCCAGAAATTTGGGCTCCG	17339
Db	19026	GCAAGGGGCGACAGTGGAGGGGCTCTCTCTAGTGGGCTCTGCCAGAAATTTGGGCTCCG	19085
QY	17340	AGTGACGGGGTCTATCTTTTGGATTTCTGACTGAAGGACACATCAGAAAACAGGACATTAT	17399
Db	19086	AGTGACGGGGTCTATCTTTTGGATTTCTGACTGAAGGACACATCAGAAAACAGGACATTAT	19145
QY	17400	TTCTCTTAGGATTCCGACTTAGGGGCGAGAGTGCAGAACTCTGCAAGATTTTAAAGGGGCT	17459
Db	19146	TTCTCTTAGGATTCCGACTTAGGGGCGAGAGTGCAGAACTCTGCAAGATTTTAAAGGGGCT	19205
QY	17460	GACTTTTACTTCCAGGGGCTCCGAATGAGAGTGGCCAGCCACTGGATTAAATATATGTA	17519

Db	19206	GACTTTTACTTCCAGGGGCTCCGAATGAGAGTGGCCAGCCACTGGATTAAATATATGTA	19265
QY	17520	TGAGCAACTTTGATTCCTTTTTTTTTTTTTTTTTTTTGTGAAAGGAGTTAGTCTTGTGCCCAAGGCT	17579
Db	19266	TGAGCAACTTTGATTCCTTTTTTTTTTTTTTTTTTTTGTGAAAGGAGTTAGTCTTGTGCCCAAGGCT	19325
QY	17580	GGAGTGCATATGCGCGATCTCGGCTCAGTCAACCTCCGCCCTCCGGGTTTAAAGCAATTC	17639
Db	19326	GGAGTGCATATGCGCGATCTCGGCTCAGTCAACCTCCGCCCTCCGGGTTTAAAGCAATTC	19385
QY	17640	TCCCGTCTCAGCTCTCTGAGTAGCTGGGATTACAGGCTCCCGCCACACACTCAGCTGAT	17699
Db	19386	TCCCGTCTCAGCTCTCTGAGTAGCTGGGATTACAGGCTCCCGCCACACACTCAGCTGAT	19445
QY	17700	TTTTGTATTTTTAGTAGAGACCGGGTTTCGCCACGTTGGCCAGGCTGGTCTGGAACTCT	17759
Db	19446	TTTTGTATTTTTAGTAGAGACCGGGTTTCGCCACGTTGGCCAGGCTGGTCTGGAACTCT	19505
QY	17760	GACCTCAGGTGATCCACCCGCTTCGGCTCCCAAAAGTGTGGGATTAACAGGGCGTGAGCCA	17819
Db	19506	GACCTCAGGTGATCCACCCGCTTCGGCTCCCAAAAGTGTGGGATTAACAGGGCGTGAGCCA	19565
QY	17820	CCACGCCAGCTGCAACTTTTGATTCTTAGTAGAAAGCCAGAAATTCATCTGTGTGAGT	17879
Db	19566	CCACGCCAGCTGCAACTTTTGATTCTTAGTAGAAAGCCAGAAATTCATCTGTGTGAGT	19625
QY	17880	GGCTGTGAAAGAGATTTTGGTGTTCCTGGATTTTCAGGCGAATGGTGGGCTTCAGTCTTC	17939
Db	19626	GGCTGTGAAAGAGATTTTGGTGTTCCTGGATTTTCAGGCGAATGGTGGGCTTCAGTCTTC	19685
QY	17940	AAATCTGAGAAAGCGGGGCGCAACACGCTGTCTGATAGTTGGCGGTGGTCTGGCGGGTG	17999
Db	19686	AAATCTGAGAAAGCGGGGCGCAACACGCTGTCTGATAGTTGGCGGTGGTCTGGCGGGTG	19745
QY	18000	GAGATTCTGAGTAGCAGGATTTAGCACCTTAGGGGCTCTCCAGGGATGGTGGCTAGTGCT	18059
Db	19746	GAGATTCTGAGTAGCAGGATTTAGCACCTTAGGGGCTCTCCAGGGATGGTGGCTAGTGCT	19805
QY	18060	CTGAATTTCTGGTGGGTGCACTCTGAAACCTTCACAGCTGTCTCTGAGTGATCAGGAAAG	18119
Db	19806	CTGAATTTCTGGTGGGTGCACTCTGAAACCTTCACAGCTGTCTCTGAGTGATCAGGAAAG	19865
QY	18120	AAATTTCTCTACTCTGGGTAGATGGATCCCGCTCTTAAGCCCATGCACTTCTCCGAGGA	18179
Db	19866	AAATTTCTCTACTCTGGGTAGATGGATCCCGCTCTTAAGCCCATGCACTTCTCCGAGGA	19925
QY	18180	CGCGCTGTATTTCTGATGGAGTACGTCAACCGGGGAGACTTTGATGTACCAATTCAACA	18239
Db	19926	CGCGCTGTATTTCTGATGGAGTACGTCAACCGGGGAGACTTTGATGTACCAATTCAACA	19985
QY	18240	GCTGGCAAGTTTAAAGGAGCCCATGACAGCTGAGTCTCGGCCAACAGAGAAATGGTCGGG	18299
Db	19986	GCTGGCAAGTTTAAAGGAGCCCATGACAGCTGAGTCTCGGCCAACAGAGAAATGGTCGGG	20045
QY	18300	GTGGTGAAGGGGCGAGGATCCAGCCACTGACCTTCTGACGCTCCCGCCACCCCGCTCT	18359
Db	20046	GTGGTGAAGGGGCGAGGATCCAGCCACTGACCTTCTGACGCTCCCGCCACCCCGCTCT	20105
QY	18360	CCAGGTTCTACGCGCAGAAATCGGTATCGGCTCTTCTTCTTACATCAGGGGATCA	18419
Db	20106	CCAGGTTCTACGCGCAGAAATCGGTATCGGCTCTTCTTCTTACATCAGGGGATCA	20165
QY	18420	TCTACAGGTGAGCAGCCCGAGGAATTTCCGTGGAGGAAATACGCCCTCTGGAAGGGAAGG	18479
Db	20166	TCTACAGGTGAGCAGCCCGAGGAATTTCCGTGGAGGAAATACGCCCTCTGGAAGGGAAGG	20225
QY	18480	GATTTGAAATATGTGGCTCTAGACTGCTGAACTCAACACTTCTTGCAATTCCTGCCCCACA	18539
Db	20226	GATTTGAAATATGTGGCTCTAGACTGCTGAACTCAACACTTCTTGCAATTCCTGCCCCACA	20285
QY	18540	CCCCTGCAATCGTCCAGGAGCTGAAAGCTGGACAATGTGATGCTGGATGCTGAGGAGACA	18599













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Qy 13364 TAGAGGCTGCAGTGTAGCCAGATCGCTCACTGCACTCCAGCGTGGATGACAGAGGGAGA 13423
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 14239 CAGAGGTTGCAGTGTAGCTGAGACTGCATCCTCAACCTGGGTGACAAAAGGAGA 14180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 13424 CTCTGTCTCAAAAAAAGAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAG 13483
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 14179 TTCTGTCTCAAAAAAAGAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAG 14120
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Qy 13484 GCAACAAATGTTATGATCTTTACTGGACTCTTACAGAACTTTACAGAGTTTTTAAT 13543
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 14119 GAATGAATGAATGGAGAGATTAAAGATGATCATGCTTGTAGATT----- 14076
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 13544 GTTGTGTGTGGGGTTACCTGCATCAGAAATTCCTAGAGTGTCTTTTAAAGACAT 13603
Db ----- 14075
Qy 13604 TCCCAGCGCTTTCGACAGACTTACTCAGTGAGATCTCTCTGATGCCTCAAAATGTCTGCC 13663
Db ----- 14075
Qy 13664 TACTAAATTAATTCCTCAGGTGATCCTTTTGCAAAGTTAAGTTTGAGAAATGGGCTCTGCC 13723
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Qy 14075 -----TTTAAAACTCAAGAAATCG 14057
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Qy 13724 GCCGGGCGAGTGGCTCAGCGCTGTCTATCCAGCACTTTGGGAGCCCAAGGGGGTGGAT 13783
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Qy 14056 GCTGGGTGTGGTGTACGCTGTAATCCAGCACTTTGGGAGGCTGAGGGGGTGGAT 13997
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 13784 CACGAGGTCAGGAGATCAGACCATCTCTGGCTTAACACCGTGAATCCCGTCTCTACTAAA 13843
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 13996 CACCAGGTCAGGAGATCAGACCATCTCTGGCTTAACACCGTGAATCCCGTCTCTACTAAA 13937
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Qy 13844 AATACAAAAAATTAGTGTGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 13903
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Qy 13904 CTGAGGAGGAGAAATGGCATGAACCTGGAGGTGGAGCTTGCAATGAGCCGAGATCGTGC 13963
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 13877 CTGATGCAGGAGAAATGGCGTGAACCCAGAGCGGAGCTTGCAATGAGCCGAGATCGCAC 13818
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Qy 13964 CACTGCATACAGCGCTGGGTGACAGAGCGAGACTCTATCTCAGAAAAAATAAAAAA 14020
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 13817 CACTGCATCTCCAGCGCTGGCGGTGACAGCGAGACTCCGTCTCAAAAAAATAAAAAA 13761
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Search completed: October 20, 2006, 09:33:50  
Job time : 525 secs

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RESULT 1
US-10-684-042-18
; Sequence 18, Application US/10684042
; GENERAL INFORMATION:
; APPLICANT: BULLERDIEK, Jörn
; APPLICANT: RIPPE, Volkhard
; APPLICANT: BELGE, Gazanfer
; APPLICANT: MEIBOOM, Maren
; TITLE OF INVENTION: Nucleic acid sequences of hyperplasias and tumors of the thyroid
; FILE REFERENCE: BEL-100US
; CURRENT APPLICATION NUMBER: US/10/684,042
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: PCT/EP02/04090
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: DE10118452.2
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 24801
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Genomic organisation of PKCG contained in BAC clone Acc.:
; OTHER INFORMATION: AC008440 (Homo sapiens chromosome 19 clone CTC-331H23, complete

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US-10-684-042-18

Query Match		98.0%;	Score 24801;	DB 1;	Length 24801;	
Best Local Similarity		100.0%;	Pred. No. 0;			
Matches 24801;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	257	GGCGCGCGGGGTGCGGCTCCCTGCGCGCGCTCGCGACCTCGAGGTGCTTGGCCC	316			
DB	1	GGCGCGCGGGGTGCGGCTCCCTGCGCGCGCTCGCGACCTCGAGGTGCTTGGCCC	60			
QY	317	TCTCTGCCCACTCGGAATTTCCCTGTGGCTCCCTTTGATCCTTCGAGTCTCCAGCTCCT	376			
DB	61	TCTCTGCCCACTCGGAATTTCCCTGTGGCTCCCTTTGATCCTTCGAGTCTCCAGCTCCT	120			
QY	377	CTCCCTTCACCTGTTTCCCCCAAGAAAGGAGGATCTGTGCTCCCTGCTAGCTTCTGGG	436			
DB	121	CTCCCTTCACCTGTTTCCCCCAAGAAAGGAGGATCTGTGCTCCCTGCTAGCTTCTGGG	180			
QY	437	GCATGGCTGTGTCGGGCCCGCGGTAGCGGATTCAGAGGGGGGACCCCGGCCCTGTGTT	496			
DB	181	GCATGGCTGTGTCGGGCCCGCGGTAGCGGATTCAGAGGGGGGACCCCGGCCCTGTGTT	240			
QY	497	TGCAGAAAGGGGCGCTCGAGGCAGAAAGTGTGTCCACGAAGTCAAGAGGCCACAAGTTACC	556			
DB	241	TGCAGAAAGGGGCGCTCGAGGCAGAAAGTGTGTCCACGAAGTCAAGAGGCCACAAGTTACC	300			
QY	557	GCTCGCTTCTCAAGAGCCCACTTCTGACGCCACTGCAACGACTTCACTGTGTGAGGG	616			
DB	301	GCTCGCTTCTTCAAGCAGCCCACTTCTGACGCCACTGCAACGACTTCACTGTGTGAGGG	360			
QY	617	AAGGGGGCTGGGGGACTGGGGACAGAGGACTAGGGGTGAGACTCTCTATCACGCCGAC	676			
DB	361	AAGGGGGCTGGGGGACTGGGGACAGAGGACTAGGGGTGAGACTCTCTATCACGCCGAC	420			
QY	677	CCCTGTGGAAGGAAGAGAGGGGCTGTAGTCCCGACTCCAGAGTCTAGGATGGCCAG	736			
DB	421	CCCTGTGGAAGGAAGAGAGGGGCTGTAGTCCCGACTCCAGAGTCTAGGATGGCCAG	480			
QY	737	GGAACTGGAGCTTGCATCTCTGGTTTCACTGAGGAGGAGGCTGTTCTGTGAGTGC	796			
DB	481	GGAACTGGAGCTTGCATCTCTGGTTTCACTGAGGAGGAGGCTGTTCTGTGAGTGC	540			
QY	797	TGGGTCCGAGGAGGAGGAGGCTGGAGGACAGAGTCTCTGGGTCTGAGGAG	856			
DB	541	TGGGTCCGAGGAGGAGGAGGCTGGAGGACAGAGTCTCTGGGTCTGAGGAG	600			
QY	857	GAAAGGCTGGGGGCTGGAGCTTGGATTCCTGGGTCTGAAGGAGGAAGAACTGGGGG	916			
DB	601	GAAAGGCTGGGGGCTGGAGCTTGGATTCCTGGGTCTGAAGGAGGAAGAACTGGGGG	660			
QY	917	CTGAATCTCAGTCTAAGGGAAGAGGCTGGGGGCCAAAATTTCTGGGTCTAGAAAGAG	976			
DB	661	CTGAATCTCAGTCTAAGGGAAGAGGCTGGGGGCCAAAATTTCTGGGTCTAGAAAGAG	720			
QY	977	GAGGTGGCGGGGCTTGGACACTGGGCGCTCGGGAGGAGGCTCAGAGAGCGCAGGGCC	1036			
DB	721	GAGGTGGCGGGGCTTGGACACTGGGCGCTCGGGAGGAGGCTCAGAGAGCGCAGGGCC	780			
QY	1037	CCTGTGGCTCGCAGAGGTTGGGGTCCAGGTAACCCCTTTCTGCACTGACCTAGGATCCCT	1096			
DB	781	CCTGTGGCTCGCAGAGGTTGGGGTCCAGGTAACCCCTTTCTGCACTGACCTAGGATCCCT	840			
QY	1097	GACTCTTCAGGGGTATCGGAAGCAGAGGCTCGCAATGTCAAGGTAAAGCTGGGGACCG	1156			
DB	841	GACTCTTCAGGGGTATCGGAAGCAGAGGCTCGCAATGTCAAGGTAAAGCTGGGGACCG	900			
QY	1157	GGGCTCTCTGGGACCTCTCAGAGGGGTGGAGGCTGGGGCCCCCACAGCTGAGGCTGTGACA	1216			
DB	901	GGGCTCTCTGGGACCTCTCAGAGGGGTGGAGGCTGGGGCCCCCACAGCTGAGGCTGTGACA	960			
QY	1217	CACGTGTTCTGTGTTCCCAAGAGCGCGGGGAGCCCGGGCGGGGGGTGTGGCAGAG	1276			
DB	961	CACGTGTTCTGTGTTCCCAAGAGCGCGGGGAGCCCGGGCGGGGGGTGTGGCAGAG	1020			

QY	1277	ACACAGCTCTGTGTGGGAGGAGCTTTGATGTGGGGCCACCGCGAGGTGTGTCTGGG	1336
DB	1021	ACACAGCTCTGTGTGGGAGGAGCTTTGATGTGGGGCCACCGCGAGGTGTGTCTGGG	1080
QY	1337	GGCCCTCTCCCTCGGCGGCTCCAGGTGGGACAGATATTTGGAGAAATCTGTGTCCATGGG	1396
DB	1081	GGCCCTCTCCCTCGGCGGCTCCAGGTGGGACAGATATTTGGAGAAATCTGTGTCCATGGG	1140
QY	1397	AACATGAGATTTGGAAGAGGAGCTGAAGGGGGAGAGGGGGCTGGAGATGCA	1456
DB	1141	AACATGAGATTTGGAAGAGGAGCTGAAGGGGGAGAGGGGGCTGGAGATGCA	1200
QY	1457	AAGTCAAGAGCCCCCCCCACCCAGGCTGCCCTGCCATCAACACAGCCGCTCTAGG	1516
DB	1201	AAGTCAAGAGCCCCCCCCACCCAGGCTGCCCTGCCATCAACACAGCCGCTCTAGG	1260
QY	1517	CAGGGCAGGCGCGGTGGGTCAACAAATGGGCGAGTGGGGGCGGGCGGGCGGCAAGTT	1576
DB	1261	CAGGGCAGGCGCGGTGGGTCAACAAATGGGCGAGTGGGGGCGGGCGGGCGGCAAGTT	1320
QY	1577	CTGGGGCGGAGAGAGGGGGCGAGTCTTGAGCACAGCTGCTACTGCTGAGNACAGAG	1636
DB	1321	CTGGGGCGGAGAGAGGGGGCGAGTCTTGAGCACAGCTGCTACTGCTGAGNACAGAG	1380
QY	1637	TGAGTCAAGGTGGGGGCGGGCGGAGCAGCGCCCCCAGACTCACCTTCTGCCCAAGTTG	1696
DB	1381	TGAGTCAAGGTGGGGGCGGGCGGAGCAGCGCCCCCAGACTCACCTTCTGCCCAAGTTG	1440
QY	1697	CTGCTTCTCGGGCTCGGTCTGAAGATATTTGGTTCGTTTCGTTTGAATCTGTCTGCTC	1756
DB	1441	CTGCTTCTCGGGCTCGGTCTGAAGATATTTGGTTCGTTTTCGTTTGAATCTGTCTGCTC	1500
QY	1757	TCTCTGGCTTCTGATCTCGGTCCGTGGGCTGTGCTCTTCTGTCATCGGATCTCTATT	1816
DB	1501	TCTCTGGCTTCTGATCTCGGTCCGTGGGCTGTGCTCTTCTGTCATCGGATCTCTATT	1560
QY	1817	TTCTTCTCTCTTTTCCATCTCCCTGCTGAGCTCTGCTCTGCTCTCTCTGTAAG	1876
DB	1561	TTCTTCTCTCTTTTCCATCTCCCTGCTGAGCTCTGCTCTGCTCTCTCTGTAAG	1620
QY	1877	TCTCTGGCTCTGTCTGACTGAGCCCATCTCTTGGGTTTCTGTCTCTCTCTCTCTC	1936
DB	1621	TCTCTGGCTCTGTCTGACTGAGCCCATCTCTTGGGTTTCTGTCTCTCTCTCTCTC	1680
QY	1937	TCTCTGGCTCCGATTTCTCTCTGTGGACTCTCTGTGTGAGATCCCTCTCTCTCTCGG	1996
DB	1681	TCTCTGGCTCCGATTTCTCTCTGTGGACTCTCTGTGTGAGATCCCTCTCTCTCTCTCGG	1740
QY	1997	TTTTCTCAGTGTCCGAGTTCGGCTCTCTCTTTTCCAAATTTCTGTCTCTGGGTCCTCCG	2056
DB	1741	TTTTCTCAGTGTCCGAGTTCGGCTCTCTCTTTTCCAAATTTCTGTCTCTGGGTCCTCCG	1800
QY	2057	CTGACTTAATCCATGCTCTGTCTCTATGATTTTCACTATAGTCTGAGCTTT	2116
DB	1801	CTGACTTAATCCATGCTCTGTCTCTATGATTTTCACTATAGTCTGAGCTTT	1860
QY	2117	GTGTTTCATCGAGTSCCAGAAATTTGTGACTTTCAGTGTCCAGGCTGGGAAGGGC	2176
DB	1861	GTGTTTCATCGAGTSCCAGAAATTTGTGACTTTCAGTGTCCAGGCTGGGAAGGGC	1920
QY	2177	CCCCAGACGAGTGTGCTCGGACACCTGGTTCCTCTCTGGGCGCTGCCCCCGGCC	2236
DB	1921	CCCCAGACGAGTGTGCTCGGACACCTGGTTCCTCTCTGGGCGCTGCCCCCGGCC	1980
QY	2237	TCACCCCTCGGCTCCGTCCCAATTTCTCTGCTATTTTATGCTGGGAGGGGAGGGG	2296
DB	1981	TCACCCCTCGGCTCCGTCCCAATTTCTCTGCTATTTTATGCTGGGAGGGGAGGGG	2040
QY	2297	GGCTGGAGAGATAGGGGAGCTATCTGGCCAGATTCCTTGGCCCTTGGCTGGAAAGGGG	2356
DB	2041	GGCTGGAGAGATAGGGGAGCTATCTGGCCAGATTCCTTGGCCCTTGGCTGGAAAGGGG	2100



Db 4261 TAAAAAATAATGTTTTGTAGAGATGGAGTCTCACTCACTATATTTGCCAGGCTGGTCTT 4320  
QY 4577 CAACTCTGGTCTCACTCGAATCTCTGCTCAGCTCCCAAAATGATGGATTAACAGC 4636  
Db 4321 CAACTCCTGGTCTCACTCGAATCTCTGCTCAGCTCCCAAAATGATGGATTAACAGC 4380  
QY 4637 GTGAGCACTGACCTGGCTCAAGTATTTGTATACAGTATAGTTGATCCACACAAC 4696  
Db 4381 GTGAGCACTGACCTGGCTCAAGTATTTGTATACAGTATAGTTGATCCACACAAC 4440  
QY 4697 AGCTTATTTGGTTATTTTCCCTGCTCTAFTCTGGTTGAATCCAGCTCCACACTTTTG 4756  
Db 4441 AGCTTATTTGGTTATTTTCCCTGCTCTAFTCTGGTTGAATCCAGCTCCACACTTTTG 4500  
QY 4757 GTTCTGTGACATTTCTGAGTTAAATTTACCTCTCTGCACTGTTGAATCTCTGTTGTA 4816  
Db 4501 GTTCTGTGACATTTCTGAGTTAAATTTACCTCTCTGCACTGTTGAATCTCTGTTGTA 4560  
QY 4817 AAGTGGAGATGAATAATTTATGCTCACTATGGAATGTTTGAAGATTTAGTGAATCAGACAT 4876  
Db 4561 AAGTGGAGATGAATAATTTATGCTCACTATGGAATGTTTGAAGATTTAGTGAATCAGACAT 4620  
QY 4877 TTGGATGGTTTCTGACACATAGCAAGAGCCAAAATATTTATTTTCTTTGTTAAAT 4936  
Db 4621 TTGGATGGTTTCTGACACATAGCAAGAGCCAAAATATTTATTTTCTTTGTTAAAT 4680  
QY 4937 TATTTATGACCAATGAGGAACGAGTGAATAGTGAGAGAGATCTTCTCTGCAATC 4996  
Db 4681 TATTTATGACCAATGAGGAACGAGTGAATAGTGAGAGAGATCTTCTCTGCAATC 4740  
QY 4997 ACTCGGGGGTTTTTTTGTGTTTTTTTTTTTTTGTGTTGAGACAGGGTCTCACTCTGTTG 5056  
Db 4741 ACTCGGGGGTTTTTTTGTGTTTTTTTTTTTTTGTGTTGAGACAGGGTCTCACTCTGTTG 4800  
QY 5057 CCCAGGCTGGAGTCAATAGTCTATCACTGCTCACTGCACTGCTGCACTGCGGGCTCA 5116  
Db 4801 CCCAGGCTGGAGTCAATAGTCTATCACTGCTCACTGCACTGCTGCACTGCGGGCTCA 4860  
QY 5117 AGTGATTCAGTCTGGCAGTTGATCTTTAAAGTAACTACATGCGCCAGGACAGTGGC 5176  
Db 4861 AGTGATTCAGTCTGGCAGTTGATCTTTAAAGTAACTACATGCGCCAGGACAGTGGC 4920  
QY 5177 TCACGCTGTAACTCCAAACACTTTGGGAGCCGAGCGGGTGGATCACTGAGGTTGGGA 5236  
Db 4921 TCACGCTGTAACTCCAAACACTTTGGGAGCCGAGCGGGTGGATCACTGAGGTTGGGA 4980  
QY 5237 GTTCGAGACCAAGCTGACCAACATGGAGAACCAAGTGTCTACTAAGAAATACAAATTTAG 5296  
Db 4981 GTTCGAGACCAAGCTGACCAACATGGAGAACCAAGTGTCTACTAAGAAATACAAATTTAG 5040  
QY 5297 CTGGGGTGGTGACACAGCCTGTAATCCAGCTACTCAGGAGGCTGAGGACAGGAGATC 5356  
Db 5041 CTGGGGTGGTGACACAGCCTGTAATCCAGCTACTCAGGAGGCTGAGGACAGGAGATC 5100  
QY 5357 ACTTGAACCCAGAGCGGAGGTTGCACTGAGCCCAAGATTTGCGCAATTTGCACTCCAGCT 5416  
Db 5101 ACTTGAACCCAGAGCGGAGGTTGCACTGAGCCCAAGATTTGCGCAATTTGCACTCCAGCT 5160  
QY 5417 GGGCAGCAAGAACAAACCTCTCTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 5476  
Db 5161 GGGCAGCAAGAACAAACCTCTCTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 5220  
QY 5477 AAAAGGTAAATGATGCTTGAACAGGATGTTGCTCATGCTGTAATCCAGCTCTTTGGG 5536  
Db 5221 AAAAGGTAAATGATGCTTGAACAGGATGTTGCTCATGCTGTAATCCAGCTCTTTGGG 5280  
QY 5537 AGGCTGAGCAAGCGGATCAGCGAGTCAAGAGATCCAAACCACTCTGCGTAAACGCGGTGA 5596  
Db 5281 AGGCTGAGCAAGCGGATCAGCGAGTCAAGAGATCCAAACCACTCTGCGTAAACGCGGTGA 5340  
QY 5597 AACCCCGTCTCTACTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 5656  
Db 5341 AACCCCGTCTCTACTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 5400

QY 5657 CCCAGCTACTCGGAGGCTGAGGAGGATCGCTTTGAACCCCGAGGACAGAGTTGCA 5716  
Db 5401 CCCAGCTACTCGGAGGCTGAGGAGGATCGCTTTGAACCCCGAGGACAGAGTTGCA 5460  
QY 5717 GTGAGCGAGATCAACACACTGCACTCTAGCTCGGCGACAGAGTGAAGTCCATCTCAA 5776  
Db 5461 GTGAGCGAGATCAACACACTGCACTCTAGCTCGGCGACAGAGTGAAGTCCATCTCAA 5520  
QY 5777 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 5836  
Db 5521 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 5580  
QY 5837 CCCAGGAGGAGGACATGCCCCCACTTTTCAAGCGGTAAATCTCAGGCTTTGAAAAGGGG 5896  
Db 5581 CCCAGGAGGAGGACATGCCCCCACTTTTCAAGCGGTAAATCTCAGGCTTTGAAAAGGGG 5640  
QY 5897 CAGCGTGGTGAAGGCCACCTAGCTGGGTAGGGATAGAGGCAAGATTTGAACTCTGTATGT 5956  
Db 5641 CAGCGTGGTGAAGGCCACCTAGCTGGGTAGGGATAGAGGCAAGATTTGAACTCTGTATGT 5700  
QY 5957 ATGTAAACACAGCCTCCGTCTCTCTCTTTTAAACAGCGACGTTCACTTTTGAGAAATAA 6016  
Db 5701 ATGTAAACACAGCCTCCGTCTCTCTCTTTTAAACAGCGACGTTCACTTTTGAGAAATAA 5760  
QY 6017 GAACAGCAGCCTCTGTCTGTGGATGGTTGTGTGTCAGGAGCCTGCTGAGAACCTTCAC 6076  
Db 5761 GAACAGCAGCCTCTGTCTGTGGATGGTTGTGTGTCAGGAGCCTGCTGAGAACCTTCAC 5820  
QY 6077 ACACAGCATCTTATTTAGTGGCGAGAAACCTTTTGATTTAGGTTAGGTTAGGTTAGTTA 6136  
Db 5821 ACACAGCATCTTATTTAGTGGCGAGAAACCTTTTGATTTAGGTTAGGTTAGGTTAGTTA 5880  
QY 6137 GAAGCCAGCAGACATTTGAAAAGGATCCCTGGAAACTGCCAACCCCTCTCTACCCCAATAT 6196  
Db 5881 GAAGCCAGCAGACATTTGAAAAGGATCCCTGGAAACTGCCAACCCCTCTCTACCCCAATAT 5940  
QY 6197 ATATTTCAAACTAGAAAAACCCCACTAAACATAGATGAAAAATCCAAAGATGGCTTAAATGTTCA 6256  
Db 5941 ATATTTCAAACTAGAAAAACCCCACTAAACATAGATGAAAAATCCAAAGATGGCTTAAATGTTCA 6000  
QY 6257 CCCTGTGATTAATCTCTTTTAAATGGATCTTTAGAATCAAGATTTATTTAAACAGCAGATTTGT 6316  
Db 6001 CCCTGTGATTAATCTCTTTTAAATGGATCTTTAGAATCAAGATTTATTTAAACAGCAGATTTGT 6060  
QY 6317 CCCGGGGTGTAGTGGTGGCGAGGAGAGGAGTCTCACTGATGACCTGATTTCTTTC 6376  
Db 6061 CCCGGGGTGTAGTGGTGGCGAGGAGAGGAGTCTCACTGATGACCTGATTTCTTTC 6120  
QY 6377 TTAATGGACCTCTGAAAATTTAGCAATTTGCTTTCAAAATATAGATTTATTTTCCACTTGAC 6436  
Db 6121 TTAATGGACCTCTGAAAATTTAGCAATTTGCTTTCAAAATATAGATTTATTTTCCACTTGAC 6180  
QY 6437 AGAGGAGATGCTGAGGCTCAAACTCGGAAATGAACCTTGGCCCAATCAACAGCAGTGA 6496  
Db 6181 AGAGGAGATGCTGAGGCTCAAACTCGGAAATGAACCTTGGCCCAATCAACAGCAGTGA 6240  
QY 6497 AGCGGCTGTAGCTCTTACTTACATTCAGGCTTATCTAGGACTTCAATAAATAATCCCTAACA 6556  
Db 6241 AGCGGCTGTAGCTCTTACTTACATTCAGGCTTATCTAGGACTTCAATAAATAATCCCTAACA 6300  
QY 6557 ATAAACCAAGTAAATGATTTGGGAGCATCTAAACCTGTGTAGGCAAGCTATGTTTGTATCA 6616  
Db 6301 ATAAACCAAGTAAATGATTTGGGAGCATCTAAACCTGTGTAGGCAAGCTATGTTTGTATCA 6360  
QY 6617 CCAATTTATTTTATGAGCCTCTGGGTTCTTATTAATCACTGAGAGGTCATGTTCTCCAT 6676  
Db 6361 CCAATTTATTTTATGAGCCTCTGGGTTCTTATTAATCACTGAGAGGTCATGTTCTCCAT 6420  
QY 6677 TCCACCTGGAGCTCAGAGAGGCAATCCATATGACACCTGACAGAGCTGCCAGTGAAGG 6736  
Db 6421 TCCACCTGGAGCTCAGAGAGGCAATCCATATGACACCTGACAGAGCTGCCAGTGAAGG 6480

QY	6737	AGCTGGGTTT	CAGGTTG	CCCAAGTCT	CTCAATAA	TAATCT	TTGGGAGT	TTGGGGAT	6796
Db	6481	AGCTGGGTTT	CAGGTTG	CCCAAGTCT	CTCAATAA	TAATCT	TTGGGAGT	TTGGGGAT	6540
QY	6797	GGGAATAT	GGGAGT	TTGGAGTCT	CTCGCTCT	TTTATG	TTTCCCA	GATATCAT	TTGG
Db	6541	GGGAATAT	GGGAGT	TTGGAGTCT	CTCGCTCT	TTTATG	TTTCCCA	GATATCAT	TTGG
QY	6857	TCAGGAGG	CCCCCT	CTGCACT	CCCCCT	CTGCACT	CCCCCT	CTGCACT	CCCCCT
Db	6601	TCAGGAGG	CCCCCT	CTGCACT	CCCCCT	CTGCACT	CCCCCT	CTGCACT	CCCCCT
QY	6917	AGACAGAA	TTCTGT	CTATCA	TCAGGCT	GGAGT	GCAGT	GCACAA	TTCTGT
Db	6661	AGACAGAA	TTCTGT	CTATCA	TCAGGCT	GGAGT	GCAGT	GCACAA	TTCTGT
QY	6977	AACCTCGG	CTCTGG	ATTCAAGCA	TTCTAT	CGCTCAG	CTCTG	AGTAGT	GGGATT
Db	6721	AACCTCGG	CTCTGG	ATTCAAGCA	TTCTAT	CGCTCAG	CTCTG	AGTAGT	GGGATT
QY	7037	ACAGGCAT	GCACCA	CCATGTC	CCGCTA	ATTTTGT	ATTAT	TTAGTAG	AGACAGT
Db	6781	ACAGGCAT	GCACCA	CCATGTC	CCGCTA	ATTTTGT	ATTAT	TTAGTAG	AGACAGT
QY	7097	CATGTTGC	TAGCTG	TCGGAA	CTCTG	AGCTCA	AGGCAAT	CCGCCAC	CTCGGCTC
Db	6841	CATGTTGC	TAGCTG	TCGGAA	CTCTG	AGCTCA	AGGCAAT	CCGCCAC	CTCGGCTC
QY	7157	CCAAAGT	CTGGGAT	TACAGCAT	AGCCAC	CGCAGC	CCAGC	AGCAGC	CGGATTTAAA
Db	6901	CCAAAGT	CTGGGAT	TACAGCAT	AGCCAC	CGCAGC	CCAGC	AGCAGC	CGGATTTAAA
QY	7217	ATTTCAT	CCCCCA	CTTCTG	TGGTCC	CAATCT	CGCTCA	TTTTTCT	CCAGAGCACC
Db	6961	ATTTCAT	CCCCCA	CTTCTG	TGGTCC	CAATCT	CGCTCA	TTTTTCT	CCAGAGCACC
QY	7277	CATTACCA	CCATCA	AACTAT	ATGTTT	ATTTA	TTTAC	CAATGTT	TACATCTG
Db	7021	CATTACCA	CCATCA	AACTAT	ATGTTT	ATTTA	TTTAC	CAATGTT	TACATCTG
QY	7337	CCATTAGG	AGTAACT	CCCATG	TGACAA	AGAGT	TTTTTTT	TTTTCAT	TGTTAA
Db	7081	CCATTAGG	AGTAACT	CCCATG	TGACAA	AGAGT	TTTTTTT	TTTTCAT	TGTTAA
QY	7397	GGTCCCA	CCACCA	AGACAG	TCCTG	GGCACA	CAGCAG	GTGCT	CAATGATT
Db	7141	GGTCCCA	CCACCA	AGACAG	TCCTG	GGCACA	CAGCAG	GTGCT	CAATGATT
QY	7457	AGAGTGA	AGAGAT	GGAGCT	CTCAGG	CTGAC	CTAGAG	CAAGC	AGGAGATA
Db	7201	AGAGTGA	AGAGAT	GGAGCT	CTCAGG	CTGAC	CTAGAG	CAAGC	AGGAGATA
QY	7517	AGGCCCC	CTCCCT	GGGTTT	TTAGGAC	CTTCC	CAAGC	CCCCCT	TAAGCAGT
Db	7261	AGGCCCC	CTCCCT	GGGTTT	TTAGGAC	CTTCC	CAAGC	CCCCCT	TAAGCAGT
QY	7577	CCCCAGG	ACCCCG	GAACAA	CAAGT	TTCCG	CTGAT	AGCTAC	AGCAGC
Db	7321	CCCCAGG	ACCCCG	GAACAA	CAAGT	TTCCG	CTGAT	AGCTAC	AGCAGC
QY	7637	TGGGAC	CACTGT	GGCTCT	CTCTA	CGGCTTT	GTGCA	CCAGGCA	TGAATG
Db	7381	TGGGAC	CACTGT	GGCTCT	CTCTA	CGGCTTT	GTGCA	CCAGGCA	TGAATG
QY	7697	GAGTGAC	CTGGG	CTTTG	CCAGG	CCCTT	CCAA	AGCCCG	GTGCGG
Db	7441	GAGTGAC	CTGGG	CTTTG	CCAGG	CCCTT	CCAA	AGCCCG	GTGCGG
QY	7757	CCGGGAT	GGG	GGTGG	AGTCT	TTGGCT	TTGGG	GGCGG	CTGAGG
Db	7501	CCGGGAT	GGG	GGTGG	AGTCT	TTGGCT	TTGGG	GGCGG	CTGAGG
QY	7817	GCTTTCC	CTCCAG	GGCTGC	GAGTGA	ACGTC	AGC	CGGCG	CTGTG

Db	7561	GCTTTCC	CTCCAG	CTGCG	AGATGA	ACCTG	CCGCG	CTGTG	CTAGCTG
QY	7877	CTGTG	CGGTG	TGG	ACAC	CCGAG	CGCG	CGCTC	AGCTG
Db	7621	CTGTG	CGGTG	TGG	ACAC	CCGAG	CGCG	CGCTC	AGCTG
QY	7937	CACAG	CAGAT	GAAT	CCAC	GTAA	CTGGT	GAGG	CCCG
Db	7681	CACAG	CAGAT	GAAT	CCAC	GTAA	CTGGT	GAGG	CCCG
QY	7997	TCGCC	CAAGT	GTG	AGG	GGG	CTCAC	CAAG	GCAC
Db	7741	TCGCC	CAAGT	GTG	AGG	GGG	CTCAC	CAAG	GCAC
QY	8057	GATGG	GGCC	ACG	CTCT	TATG	TGTC	AC	CGCC
Db	7801	GATGG	GGCC	ACG	CTCT	TATG	TGTC	AC	CGCC
QY	8117	AGCAC	ACCC	AGCC	ATAC	CCCT	TTTGG	CTCG	AGCC
Db	7861	AGCAC	ACCC	AGCC	ATAC	CCCT	TTTGG	CTCG	AGCC
QY	8177	CTTCT	GCAC	CTG	TAA	TGAC	TTTCT	TTTTT	TGG
Db	7921	CTTCT	GCAC	CTG	TAA	TGAC	TTTCT	TTTTT	TGG
QY	8237	TGTTG	CTCA	AGCT	GGAG	TGCA	TGCG	CTCA	TCG
Db	7981	TGTTG	CTCA	AGCT	GGAG	TGCA	TGCG	CTCA	TCG
QY	8297	GTTCA	AGTCA	TCTC	CTG	CTC	AGCT	CCG	AGT
Db	8041	GTTCA	AGTCA	TCTC	CTG	CTC	AGCT	CCG	AGT
QY	8357	AAGCC	CGCT	TAAT	TTTTT	GTAT	TTTTT	TAGT	CAAA
Db	8101	AAGCC	CGCT	TAAT	TTTTT	GTAT	TTTTT	TAGT	CAAA
QY	8417	GCTCT	CGAA	CTC	TGAC	CCCG	AGT	GTAT	CCCT
Db	8161	GCTCT	CGAA	CTC	TGAC	CCCG	AGT	GTAT	CCCT
QY	8477	AACAG	CGT	GAG	CCAC	CGCG	CTG	CGCA	ATG
Db	8221	AACAG	CGT	GAG	CCAC	CGCG	CTG	CGCA	ATG
QY	8537	ATTTT	TTT	TGAG	ATG	AGT	CTT	CTG	TC
Db	8281	ATTTT	TTT	TGAG	ATG	AGT	CTT	CTG	TC
QY	8597	GCTCA	CTG	CAAT	CTC	TGCT	CCG	GGT	TC
Db	8341	GCTCA	CTG	CAAT	CTC	TGCT	CCG	GGT	TC
QY	8657	GCTGA	ATTT	TAC	AGG	CGCT	CGCC	ACAC	AT
Db	8401	GCTGA	ATTT	TAC	AGG	CGCT	CGCC	ACAC	AT
QY	8717	GACAA	GAAT	CTC	GTG	TCG	CCAG	GGT	GG
Db	8461	GACAA	GAAT	CTC	GTG	TCG	CCAG	GGT	GG
QY	8777	ACCTC	CGCT	CTC	CAG	GTTC	CAAG	CGG	TT
Db	8521	ACCTC	CGCT	CTC	CAG	GTTC	CAAG	CGG	TT
QY	8837	CAGGT	GCAT	GAC	CTG	CAAC	CGG	CTCA	TTT
Db	8581	CAGGT	GCAT	GAC	CTG	CAAC	CGG	CTCA	TTT
QY	8897	ATGCT	AGC	CGG	CTG	CTG	GAA	CTCT	CA



Db 8641 ATGCTAGCAGCGCTGCTGGAACTCCTGACCTCAGGTGATCCGCCCGCTCCGCTCCC 8700  
 QY 8957 AAAGTGTCTGGGATTTACAGGGGTGAGAACCGTCCCGGCAATGGCTTTCTGGGTATAAGGA 9016  
 Db 8701 AAAGTGTCTGGGATTTACAGGGGTGAGAACCGTCCCGGCAATGGCTTTCTGGGTATAAGGA 8760  
 QY 9017 TCTTCGAAAGGAGAGAGTACTCGTGTCTGAGGAGAGCTGTGGTTCAGTACTGTGTACATGG 9076  
 Db 8761 TCTTCGAAAGGAGAGAGTACTCGTGTCTGAGGAGAGCTGTGGTTCAGTACTGTGTACATGG 8820  
 QY 9077 CCAGGGTCCAAACTCTGGTTCCTAATGGAGAGAGGGCTCTGGATCTGATTTCAAGGGTCA 9136  
 Db 8821 CCAGGGTCCAAACTCTGGTTCCTAATGGAGAGAGGGCTCTGGATCTGATTTCAAGGGTCA 8880  
 QY 9137 CTGGTTCCGGAAGGGCTCTATGCCCTGTCCTTCCTGGTTCCTGGAGAGGTAAAGTCAATG 9196  
 Db 8881 CTGGTTCCGGAAGGGCTCTATGCCCTGTCCTTCCTGGTTCCTGGAGAGGTAAAGTCAATG 8940  
 QY 9197 AGAAACGAGACTGAGAGCTTGGAAATCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGAGCGGAGTCTCGCTG 9256  
 Db 8941 AGAAACGAGACTGAGAGCTTGGAAATCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGAGCGGAGTCTCGCTG 9000  
 QY 9257 TGACGCCAGGCTGGAGTGCAGTGGCGTAATCTCGGCTCACTGCAAGCTCCGACTCTCTGG 9316  
 Db 9001 TGACGCCAGGCTGGAGTGCAGTGGCGTAATCTCGGCTCACTGCAAGCTCCGACTCTCTGG 9060  
 QY 9317 GTTCAGCTCAATCTCCCGCTCAGGCTCTGAGTAGCTGGGACCAACAGACACCTGCCACC 9376  
 Db 9061 GTTCAGCTCAATCTCCCGCTCAGGCTCTGAGTAGCTGGGACCAACAGACACCTGCCACC 9120  
 QY 9377 AGCCCGCAGCTAATTTTTTTTTTTTTTTTTTTTTTTTTTTTGTAGTGGAGCGGGTTTCAACATTTCA 9436  
 Db 9121 AGCCCGCAGCTAATTTTTTTTTTTTTTTTTTTTTTTTTTTTGTAGTGGAGCGGGTTTCAACATTTCA 9180  
 QY 9437 CAGGATGTCTCGATCTCTCGACTTGTGATCCGCCCGCTTGGCTCCCAAAGTGTGG 9496  
 Db 9181 CAGGATGTCTCGATCTCTCGACTTGTGATCCGCCCGCTTGGCTCCCAAAGTGTGG 9240  
 QY 9497 GATTCAGGCATGAGCGCGCTGCTGGCAAGCTTGGAACTTTGATGTGATGCTGAG 9556  
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 QY 9617 AGTTGGCAGGCGCCGTAACTAATTCCTATGACCCCAATGGTCTCTCTGATCCCTATGT 9676  
 Db 9361 AGTTGGCAGGCGCCGTAACTAATTCCTATGACCCCAATGGTCTCTCTGATCCCTATGT 9420  
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 Db 9421 GAAACTGAAGCTCATCCAGACCTCTGGAACTCTGACGAAACAGAGACCCGACCGTGA 9480  
 QY 9737 AGCCAGCTTAAACCTGTGTGAATGAGACCTTTGTGTGAGTCTGGGTGACAGGAA 9796  
 Db 9481 AGCCAGCTTAAACCTGTGTGAATGAGACCTTTGTGTGAGTCTGGGTGACAGGAA 9540  
 QY 9797 GGCAATGACAGCTGACAGAGATGATCTGAGGGTCTATGAGGGTCTATGAGAGAGAGAGTGA 9856  
 Db 9541 GGCAATGACAGCTGACAGAGATGATCTGAGGGTCTATGAGGGTCTATGAGAGAGAGTGA 9600  
 QY 9857 TGGAGGGGTAGGATAGAGGAAACCCAGAAAGGGCAGAGAGATGTTGGTGGAAAGGG 9916  
 Db 9601 TGGAGGGGTAGGATAGAGGAAACCCAGAAAGGGCAGAGAGATGTTGGTGGAAAGGG 9660  
 QY 9917 AATAGAGTCAATTTGAGGAGTGGAGTGGAGATACAGAAACCGAGAGACAGCCAGACCTG 9976  
 Db 9661 AATAGAGTCAATTTGAGGAGTGGAGTGGAGATACAGAAACCGAGAGACAGCCAGACCTG 9720  
 QY 9977 TATAATTAGTCTCCATTGAAGCCCCCACTTTTAGAGTTAGACAGAGATGAGAGAGAG 10036  
 Db 9721 TATAATTAGTCTCCATTGAAGCCCCCACTTTTAGAGTTAGACAGAGATGAGAGAGAG 9780

QY 10037 AGAGAGTCTCAGAGAGGCGAGAAACCCAAAGAGAGACACAGATGGAGGAGGGAGAA 10096  
 Db 9781 AGAGAGTCTCAGAGAGGCGAGAAACCCAAAGAGAGACACAGATGGAGGAGGGAGAA 9840  
 QY 10097 GATGGGGGATGGCAGGGGAGACAGAGATCAGTTGACAGGAAAGACAGAGTGTATAGAGACCA 10156  
 Db 9841 GATGGGGGATGGCAGGGGAGACAGAGATCAGTTGACAGGAAAGACAGAGTGTATAGAGACCA 9900  
 QY 10157 GAGAGGAGAGAGGGGTACAGAGACTCAGAGAGAGAGATCTCGAGAGACAGAGACAGAG 10216  
 Db 9901 GAGAGGAGAGAGGGGTACAGAGACTCAGAGAGAGAGATCTCGAGAGACAGAGACAGAG 9960  
 QY 10217 TGGGAAGGGCGCGAGAGATGACAGGAGGAGGAGAGAGAGTCTCTAGGTTTACTTTTCA 10276  
 Db 9961 TGGGAAGGGCGCGAGAGATGACAGGAGGAGGAGAGAGTCTCTAGGTTTACTTTTCA 10020  
 QY 10277 GCCCAAAGCCCTAGCTGGAGAGAGAGCCCGGTGGGAAGGTGAGAGTGGAGACCGAC 10336  
 Db 10021 GCCCAAAGCCCTAGCTGGAGAGAGAGCCCGGTGGGAAGGTGAGAGTGGAGACCGAC 10080  
 QY 10337 AAAGCAGGAGAGAGCCCGAGCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 10396  
 Db 10081 AAAGCAGGAGAGAGCCCGAGCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 10140  
 QY 10397 GAACCGAGGGAGGAGCATGAGCTCGGCTCTGCACCCATCCACCCCACTTCTCTGACGAA 10456  
 Db 10141 GAACCGAGGGAGGAGCATGAGCTCGGCTCTGCACCCATCCACCCCACTTCTCTGACGAA 10200  
 QY 10457 CCTGAAGCCAGGGGATGTGAGAGCCCGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAG 10516  
 Db 10201 CCTGAAGCCAGGGGATGTGAGAGCCCGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAG 10260  
 QY 10517 CTCCCGCAAACGACTTCAATGGGGCCATGCTTGGGTCTCGAGGTCTCGAGGTCTCAAGGCGCC 10576  
 Db 10261 CTCCCGCAAACGACTTCAATGGGGCCATGCTTGGGTCTCGAGGTCTCGAGGTCTCAAGGCGCC 10320  
 QY 10577 CGTGATGGTGTGAGGAGCAGGGCTGGGGCTGGGGATGGAGCGCAATATTACCATCT 10636  
 Db 10321 CGTGATGGTGTGAGGAGCAGGGCTGGGGCTGGGGATGGAGCGCAATATTACCATCT 10380  
 QY 10637 CCATCTGTGTGTGTCTCTCTCCAGGCCACTGTCTTCCCTCTGCTCCCTCCAGCATGC 10696  
 Db 10381 CCATCTGTGTGTGTCTCTCTCCAGGCCACTGTCTTCCCTCTGCTCCCTCCAGCATGC 10440  
 QY 10697 GCAC 10756  
 Db 10441 GCAC 10500  
 QY 10757 ATTCTTCTCTTCTCTCCCT 10816  
 Db 10501 ATTCTTCTCTTCTCTCCCT 10560  
 QY 10817 TCTCTTCCATCTCTGT 10876  
 Db 10561 TCTCTTCCATCTCTGT 10620  
 QY 10877 TCTCCCATGGTGCCTCATCCCGCTCCCGCTCTGGTCTCCGTCTGTATGTCAAGGTAC 10936  
 Db 10621 TCTCCCATGGTGCCTCATCCCGCTCCCGCTCTGGTCTCCGTCTGTATGTCAAGGTAC 10680  
 QY 10937 AAGTTACTGAACACAGGAGGAGGCGAGTATTACAATGTGCGGTGGCGGATGTGTGACAA 10996  
 Db 10681 AAGTTACTGAACACAGGAGGAGGCGAGTATTACAATGTGCGGTGGCGGATGTGTGACAA 10740  
 QY 10997 TGCAGCCTCTCTCAGAAAGTTTGGGTACCCAGACCTGGTCTCTCAAGGGAGGCCAGCC 11056  
 Db 10741 TGCAGCCTCTCTCAGAAAGTTTGGGTACCCAGACCTGGTCTCTCAAGGGAGGCCAGCC 10800  
 QY 11057 CAGCCTCCAGGTTCAAGAGCTGGCTTTCTCTCCACCCCTGAGTGGCGCTGTCTCTGG 11116  
 Db 10801 CAGCCTCCAGGTTCAAGAGCTGGCTTTCTCTCCACCCCTGAGTGGCGCTGTCTCTGG 10860



D	13021	TACAAAAATCAGCTGGGCAATGTTGGAGGCGCTGTAAATCCCAAGCTACTCGGAAGSCTGAG	13080
Q	13337	GCAGAGAAATTCCTGGATTCGGGAAGTAGAGGCTGCAGTGAGCCAGATCGCTCCACTG	13396
D	13081	GCAGAGAAATTCCTGGATTCGGGAAGTAGAGGCTGCAGTGAGCCAGATCGCTCCACTG	13140
Q	13397	CAGCTCCAGCTGGATGACAGAGGGAGACTCTCTCTCMAAATAAATAAATAAATAAATAA	13456
D	13141	CAGCTCCAGCTGGATGACAGAGGGAGACTCTCTCTCMAAATAAATAAATAAATAAATAA	13200
Q	13457	GACAAAGATCTTCAAGATTCACAAACAGCAACAAATGTTATAGTCTTTTACTGGACTCTT	13516
D	13201	GACAAAGATCTTCAAGATTCACAAACAGCAACAAATGTTATAGTCTTTTACTGGACTCTT	13260
Q	13517	ACAGAAATCTTCAAGAGTCTTAAATGTTGTTGTTGGGGTTACCTGATCAGAAATTC	13576
D	13261	ACAGAAATCTTCAAGAGTCTTAAATGTTGTTGTTGGGGTTACCTGATCAGAAATTC	13320
Q	13577	CTAGAGTCTTCTTAAAGCAATTCCTGAGCTCTTCTGAGAGCTTCTGAGAGCTTCTGAGG	13636
D	13321	CTAGAGTCTTCTTAAAGCAATTCCTGAGCTCTTCTGAGAGCTTCTGAGAGCTTCTGAGG	13380
Q	13637	ATCTCTCTGATCGCTCAAAATGCTGCTACTAAATTAATTCCTCAGGTGATCCTTTTGA	13696
D	13381	ATCTCTCTGATCGCTCAAAATGCTGCTACTAAATTAATTCCTCAGGTGATCCTTTTGA	13440
Q	13697	AAGTTAAGTTTGAAGATGGGCTCTGCGCGCGGCGAGTGGCTCAAGCTGTCATCCAG	13756
D	13441	AAGTTAAGTTTGAAGATGGGCTCTGCGCGCGGCGAGTGGCTCAAGCTGTCATCCAG	13500
Q	13757	CAGTTTGGAGGCAAGGCGGTGGATCAGAGGTCAGGAGTCAGAGCCATCTCTGGCTA	13816
D	13501	CAGTTTGGAGGCAAGGCGGTGGATCAGAGGTCAGGAGTCAGAGCCATCTCTGGCTA	13560
Q	13817	ACACGGTGAATCCCGTCTCTACTAAAAATAAATAAATAAATAAATAAATAAATAAATAA	13876
D	13561	ACACGGTGAATCCCGTCTCTACTAAAAATAAATAAATAAATAAATAAATAAATAAATAA	13620
Q	13877	TGCTGTAGTCCAGGTAATCAGGAGGCTGAGGCGAGGAGATGGATGAACCTGGAGGT	13936
D	13621	TGCTGTAGTCCAGGTAATCAGGAGGCTGAGGCGAGGAGATGGATGAACCTGGAGGT	13680
Q	13937	GGAGCTTCAATGAGCCGAGATCTGCGCACTGCATACAGCTTGGGTGACAGAGCGAGAC	13996
D	13681	GGAGCTTCAATGAGCCGAGATCTGCGCACTGCATACAGCTTGGGTGACAGAGCGAGAC	13740
Q	13997	TCTATCTCAGAAAAAATAAAGAGAGATGGGCTCTGAGGAGACAAAGGTTACACG	14056
D	13741	TCTATCTCAGAAAAAATAAAGAGAGATGGGCTCTGAGGAGACAAAGGTTACACG	13800
Q	14057	GGAGGACATTCAGGCAAGAGGTAGATCTTTGAGATCAGCAGGATGATCCTCCC	14116
D	13801	GGAGGACATTCAGGCAAGAGGTAGATCTTTGAGATCAGCAGGATGATCCTCCC	13860
Q	14117	GTACAAACCAAGAAACCCAGAGGAGATGGTGGGCAAGGCTTAGAGGAGGAGGTG	14176
D	13861	GTACAAACCAAGAAACCCAGAGGAGATGGTGGGCAAGGCTTAGAGGAGGAGGTG	13920
Q	14177	TAGGGTGGTGTGTGCTGCTTGTGCTCAGCACTCTCCACAGTTCAGCAGGACCA	14236
D	13921	TAGGGTGGTGTGTGCTGCTTGTGCTCAGCACTCTCCACAGTTCAGCAGGACCA	13980
Q	14237	CTTAATATTTACCAATGAAACCACTCTGTGCGAAGCTTGGCTAGGTAGGCTTAAC	14296
D	13981	CTTAATATTTACCAATGAAACCACTCTGTGCGAAGCTTGGCTAGGTAGGCTTAAC	14040
Q	14297	AACACAGCAACAGAAACAGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTA	14356
D	14041	AACACAGCAACAGAAACAGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTA	14100
Q	14357	TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	14416
D	14101	TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	14160

Q	14417	TGCACTGGAGGGATCTCAGCTCACTGCAACCTCTGCTCCCGGTTCAAGCGATTCTCCT	14476
D	14161	TGCACTGGAGGGATCTCAGCTCACTGCAACCTCTGCTCCCGGTTCAAGCGATTCTCCT	14220
Q	14477	GCCTTGGCTCCCAAGTAGCTGGGACTACAGGCAATGTGCCACCATGTCTACTAATTTT	14536
D	14221	GCCTTGGCTCCCAAGTAGCTGGGACTACAGGCAATGTGCCACCATGTCTACTAATTTT	14280
Q	14537	ATATTGCTAGTAGAGATGGGCTTCGCCATGTTGGCCAGGCTGTCTTGAATCTCTGACC	14596
D	14281	ATATTGCTAGTAGAGATGGGCTTCGCCATGTTGGCCAGGCTGTCTTGAATCTCTGACC	14340
Q	14597	TCAGGTGATCTGCCACCTCGGCTCCCAAGTCTGGGATTAACAGGATCAGGCACCGC	14656
D	14341	TCAGGTGATCTGCCACCTCGGCTCCCAAGTCTGGGATTAACAGGATCAGGCACCGC	14400
Q	14657	ACCCAGGCTTCAACAAATATTTATGTAGCTCAATAGGTAGGAGTGTACTGTGCTT	14716
D	14401	ACCCAGGCTTCAACAAATATTTATGTAGCTCAATAGGTAGGAGTGTACTGTGCTT	14460
Q	14717	AGCGAAACAAAGCAGACCCCTGCTTAGGAGCTCAGAGGCAAGAGATAGTACACACA	14776
D	14461	AGCGAAACAAAGCAGACCCCTGCTTAGGAGCTCAGAGGCAAGAGATAGTACACACA	14520
Q	14777	GATAGATGTAATTTACTAAGAAATAAAGTGCAGGAAGTGTCTCAATGTGTGACCAAGG	14836
D	14521	GATAGATGTAATTTACTAAGAAATAAAGTGCAGGAAGTGTCTCAATGTGTGACCAAGG	14580
Q	14837	GGTGGTAAAGAGGAGCATCTGACCCAGTTTAAAAAGTCAAGGCGGCTTCTATGAAGTAT	14896
D	14581	GGTGGTAAAGAGGAGCATCTGACCCAGTTTAAAAAGTCAAGGCGGCTTCTATGAAGTAT	14640
Q	14897	GCTTGGTCAAGGTCTTAAAGGTTTGGGAGACAATAGAGGCAAGGAGGAGGAGAG	14956
D	14641	GCTTGGTCAAGGTCTTAAAGGTTTGGGAGACAATAGAGGCAAGGAGGAGGAGAG	14700
Q	14957	CTTTACAGGAAGACCTTAAGGCGCATCCAGAGGCTTGAAGTGGAGGAGGAGCAATGAG	15016
D	14701	CTTTACAGGAAGACCTTAAGGCGCATCCAGAGGCTTGAAGTGGAGGAGGAGCAATGAG	14760
Q	15017	TGTCAGGCGAGGCTGGTGGACCATGAGGCTGGGAGAGAGAAACCACTGCAAGTCTC	15076
D	14761	TGTCAGGCGAGGCTGGTGGACCATGAGGCTGGGAGAGAGAAACCACTGCAAGTCTC	14820
Q	15077	AGTCTCAGGCTGGCTCTGCAAGTCTGGAATTAATTTAAACACAGAGGAGGAGTGA	15136
D	14821	AGTCTCAGGCTGGCTCTGCAAGTCTGGAATTAATTTAAACACAGAGGAGGAGTGA	14880
Q	15137	AAGGTTTACAAAGCATAGGGGAGACATGACCTGGTGTATTTATTTTAAATTTGGCTCTG	15196
D	14881	AAGGTTTACAAAGCATAGGGGAGACATGACCTGGTGTATTTATTTTAAATTTGGCTCTG	14940
Q	15197	TGCTGTGTAGTAGAATGCAATTAGAAAGGCGCGCTCCATGTAGAGGAGCAAGTCTG	15256
D	14941	TGCTGTGTAGTAGAATGCAATTAGAAAGGCGCGCTCCATGTAGAGGAGCAAGTCTG	15000
Q	15257	GAAGCTGACAGCAGCTTACTTGGGCGGCTTGGGCGGCGGCGGAGGAGGAGGAGG	15316
D	15001	GAAGCTGACAGCAGCTTACTTGGGCGGCTTGGGCGGCGGCGGAGGAGGAGGAGG	15060
Q	15317	TAGAGAGGAGCCCTAGCTGAAAGCCAGGTGTCTCCCTGAGCTGGGAGCCCAATGTCA	15376
D	15061	TAGAGAGGAGCCCTAGCTGAAAGCCAGGTGTCTCCCTGAGCTGGGAGCCCAATGTCA	15120
Q	15377	CCAGAGAGCTTTTACACATTAACGATCTCAGGTCCCAAGGATTTATAGAGTTAGAA	15436
D	15121	CCAGAGAGCTTTTACACATTAACGATCTCAGGTCCCAAGGATTTATAGAGTTAGAA	15180
Q	15437	AATCTGGCAGTGGGAGCCAGCAATCTGTTTACCAAAACCTCTAGGGAATTCGGCTTAG	15496
D	15181	AATCTGGCAGTGGGAGCCAGCAATCTGTTTACCAAAACCTCTAGGGAATTCGGCTTAG	15240

QY	15497	AGGCTAAGAGCAACAGAGATTCTAGAGCTGGAGTCTTGGGTTTCAATTTCTGGCTCTGTC	15556	Db	16321	AGGATGAGGGGCGGAGGCTGTCTCCGGGCCCTGCTTATCCAGTTCTGGACATCTGC	16380
Db	15241	AGGCTAAGAGCAACAGAGATTCTAGAGCTGGAGTCTTGGGTTTCAATTTCTGGCTCTGTC	15300	QY	16637	GTTTGGGATTTCTGAGTTTATGGGCGAGGCAAGAGAACTTTTGTGCTCTCTGAGTGGGCGAGGC	16696
QY	15557	TTTTACTCTGCTGTGAGCTTGGGCGAAGTACTTAAAGTCTCTGTGCTAGTCTCTCTTCT	15616	Db	16381	GTTTGGGATTTCTGAGTTTATGGGCGAGGCAAGAGAACTTTTGTGCTCTCTGAGTGGGCGAGGC	16440
Db	15301	TTTTACTCTGCTGTGAGCTTGGGCGAAGTACTTAAAGTCTCTGTGCTAGTCTCTCTTCT	15360	QY	16697	CAGCGGATTTGTCTCTCCTCAGGGGCGTGGCCGGGGGGGGTCTTTGGGGGGCGTGGCCAG	16756
QY	15617	GTAATAAGGAAACAGATACGAGGTTTCTGGAACAGCATATGATTAAGCTATCTAAAAA	15676	Db	16441	CAGCGGATTTGTCTCTCCTCAGGGGCGTGGCCGGGGGGGGTCTTTGGGGGGCGTGGCCAG	16500
Db	15361	GTAATAAGGAAACAGATACGAGGTTTCTGGAACAGCATATGATTAAGCTATCTAAAAA	15420	QY	16757	GCCAAAGGACTCATCTGGGGGCGTGGCCAGGCGAGGGCTCAACGAGAGCGAGGCGGG	16816
QY	15677	AAAAAAGGAAAGAAAGAGCTAAGTGTGTGTAATAATAATAAACCCCTCCAGGCTAT	15736	Db	16501	GCCAAAGGACTCATCTGGGGGCGTGGCCAGGCGAGGGCTCAACGAGAGCGAGGCGGG	16560
Db	15421	AAAAAAGGAAAGAAAGAGCTAAGTGTGTGTAATAATAATAAACCCCTCCAGGCTAT	15480	QY	16817	TGAGGGGCTCTCTCGGGGCGTGGCCAGGTGGAGGACTCATCGGGGGCGTGGCCAGGCA	16876
QY	15737	GGGAGTCTAGAGAAAAATTAAGCCAAAGGACAGGGTAGAGGGTGCCCAATTTTCTCTCTCT	15796	Db	16561	TGAGGGGCTCTCTCGGGGCGTGGCCAGGTGGAGGACTCATCGGGGGCGTGGCCAGGCA	16620
Db	15481	GGGAGTCTAGAGAAAAATTAAGCCAAAGGACAGGGTAGAGGGTGCCCAATTTTCTCTCTCT	15540	QY	16877	GAGGGCTCTCTCGGGGCGTGGTCAAGCGGATGAATACTTTGGGGGGTGGTTTAGAGG	16936
QY	15797	AGCGATTCTCATCTCTTCTTCTTGGGTGCTGTCTCTTGGGAGCATTTTCTTATCGC	15856	Db	16621	GAGGGCTCTCTCGGGGCGTGGTCAAGCGGATGAATACTTTGGGGGGTGGTTTAGAGG	16680
Db	15541	AGCGATTCTCATCTCTTCTTCTTGGGTGCTGTCTCTTGGGAGCATTTTCTTATCGC	15600	QY	16937	GCGGGCTTTTGTCAAGCGATGGGATCATTAATAGGCGTGGCCAGGAGATTTGCTCCTTG	16996
QY	15857	TGTGTAAGGTCTAACTGCTCTGCTCTTTCTTCTCTTCCACAGCGGGTGCGGATGG	15916	Db	16681	GCGGGCTTTTGTCAAGCGATGGGATCATTAATAGGCGTGGCCAGGAGATTTGCTCCTTG	16740
Db	15601	TGTGTAAGGTCTAACTGCTCTGCTCTTTCTTCTCTTCCACAGCGGGTGCGGATGG	15660	QY	16997	GGGGCGAGCCAGGACAGCAGATTAATGAATGAGCGTATCCAGGCGAGTAGATTTCTCGG	17056
QY	15917	GCCCTCTTCTCTCCATCCCTTCCCTTCCCTTCTAGTCCACCGACCCCAAGCGTGTCT	15976	Db	16741	GGGGCGAGCCAGGACAGCAGATTAATGAATGAGCGTATCCAGGCGAGTAGATTTCTCGG	16800
Db	15661	GCCCTCTTCTCTCCATCCCTTCCCTTCCCTTCTAGTCCACCGACCCCAAGCGTGTCT	15720	QY	17057	AGGGCGTGTGGGGCGGATGAGTCTCTCGGGGCGTGGCCAGGCGGTGATTTCTCGGTG	17116
QY	15977	TCTTCGGGGCGAGTCCAGGAGCGCTGCACATCTCCGACTTCAGCTTCTCATGGTCTAG	16036	Db	16801	AGGGCGTGTGGGGCGGATGAGTCTCTCGGGGCGTGGCCAGGCGGTGATTTCTCGGTG	16860
Db	15721	TCTTCGGGGCGAGTCCAGGAGCGCTGCACATCTCCGACTTCAGCTTCTCATGGTCTAG	15780	QY	17117	GCATGGCTTGGCCAGGTGAATGGTCTCTCGCGAGGTGTCTGAAAGCGGTGAGTTCTCTTG	17176
QY	16037	GAATAAGCAGTTTGGGAAGTTGGATTCTCTGGGGTTCTGGGGAAAGGAGGATGTCTG	16096	Db	16861	GCATGGCTTGGCCAGGTGAATGGTCTCTCGCGAGGTGTCTGAAAGCGGTGAGTTCTCTTG	16920
Db	15781	GAATAAGCAGTTTGGGAAGTTGGATTCTCTGGGGTTCTGGGGAAAGGAGGATGTCTG	15840	QY	17177	GGGGCGTGGCCAGGTGGATGGGCTCTTGGGGGAGTGGCCAGATGCTCTTTCTCTCGGG	17236
QY	16097	TGGGAAGTCTAGATTTCTGTTCTTAGGAGAGAGTGGGGGTGGGAAGACTTGGGCTCC	16156	Db	16921	GGGGCGTGGCCAGGTGGATGGGCTCTTGGGGGAGTGGCCAGATGCTCTTTCTCTCGGG	16980
Db	15841	TGGGAAGTCTAGATTTCTGTTCTTAGGAGAGAGTGGGGGTGGGAAGACTTGGGCTCC	15900	QY	17237	AGCTTTGGTCTTGAAGTGGTGTAGCGAGTCTCTCGAAATTTTTCAGCAAGGGCGACAGTGG	17296
QY	16157	TGCATCTTCAAAATATGTTAGTTTGGCCCTTCCAGTTCTCTGAGAGGAGGATTTACAG	16216	Db	16981	AGCTTTGGTCTTGAAGTGGTGTAGCGAGTCTCTCGAAATTTTTCAGCAAGGGCGACAGTGG	17040
Db	15901	TGCATCTTCAAAATATGTTAGTTTGGCCCTTCCAGTTCTCTGAGAGGAGGATTTACAG	15960	QY	17297	AGGAGGTGCTCTTCTAGTGGGCTTGGCCAGAAATTTGGGCTCCGAGTGACGGGTCTATCAC	17356
QY	16217	ATGTGACACTCTCTTGAAGGGACGGGGCGCAAGTCAAGGCTGTCTAGTCCCTTAAAGAGA	16276	Db	17041	AGGAGGTGCTCTTCTAGTGGGCTTGGCCAGAAATTTGGGCTCCGAGTGACGGGTCTATCAC	17100
Db	15961	ATGTGACACTCTCTTGAAGGGACGGGGCGCAAGTCAAGGCTGTCTAGTCCCTTAAAGAGA	16020	QY	17357	TTTTGGATTTCTGAAGAGGACACATCAGAAACAGGACATTAATTTCTTAGAGATTGCGAC	17416
QY	16277	TGAGAGAGGGCTTGGATCCCGTTTCCCTGCTCCCTTAGGAGGGGCGAGTCTCTGTA	16336	Db	17101	TTTTGGATTTCTGAAGAGGACACATCAGAAACAGGACATTAATTTCTTAGAGATTGCGAC	17160
Db	16021	TGAGAGAGGGCTTGGATCCCGTTTCCCTGCTCCCTTAGGAGGGGCGAGTCTCTGTA	16080	QY	17417	TTAGGGGAGAGAGTCAAGCTGCAAGATTTTAAAGGGGCTGACTTTACTTCCAGGGG	17476
QY	16337	CCACTGGTTCCCAACATGAGACTGGCCCTTTTGGAACTGTGGCATAGTGTGCTGGCC	16396	Db	17161	TTAGGGGAGAGAGTCAAGCTGCAAGATTTTAAAGGGGCTGACTTTACTTCCAGGGG	17220
Db	16081	CCACTGGTTCCCAACATGAGACTGGCCCTTTTGGAACTGTGGCATAGTGTGCTGGCC	16140	QY	17477	CTCCGAATGAGAGTGGCCAGCACCTGGATTAAATAATATATGATGAGCAACTTTGATTTCC	17536
QY	16397	GAGCGAGGGCTCTGATGAGCTCTACGCCATCAAGATCTTGAATAAGGACGTGATCGTC	16456	Db	17221	CTCCGAATGAGAGTGGCCAGCACCTGGATTAAATAATATATGATGAGCAACTTTGATTTCC	17280
Db	16141	GAGCGAGGGCTCTGATGAGCTCTACGCCATCAAGATCTTGAATAAGGACGTGATCGTC	16200	QY	17537	TTTTTTTTTTTTTGAAGAGGATTTAGTCTTGTCTCCCGAGGCTGAGTGAATGCGGGA	17596
QY	16457	CAGGACGAGATGTGAGCTGACGCTGGTGGAGAAAACGTGTGCTGCGCTGGGGGCGG	16516	Db	17281	TTTTTTTTTTTTTGAAGAGGATTTAGTCTTGTCTCCCGAGGCTGAGTGAATGCGGGA	17340
Db	16201	CAGGACGAGATGTGAGCTGACGCTGGTGGAGAAAACGTGTGCTGCGCTGGGGGCGG	16260	QY	17597	TCTGGCTCACTGCAACTCCGCTCCGGGTTTAAAGCAATTTCTCCCTCTCAGCTCTCT	17656
QY	16517	GGTCTGGGGGCGGCGCCCACTTCTCACCCAGCTCCACTCCACTTCCAGACCCCGGTA	16576	Db	17341	TCTGGCTCACTGCAACTCCGCTCCGGGTTTAAAGCAATTTCTCCCTCTCAGCTCTCT	17400
Db	16261	GGTCTGGGGGCGGCGCCCACTTCTCACCCAGCTCCACTCCACTTCCAGACCCCGGTA	16320	QY	17657	GAGTAGCTGGGATTTACAGGCTCCCGCCACACACTCAGCTGATTTTGTATTTTAGTAG	17716
QY	16577	AGGATGGAGGGGCGGAGGCTGTCTCTCGGGGCGCTGCTTATCCAGTTCTCGACACTGTC	16636				

Db 17401 GAGTAGTGGGATTACAGGCTCCGCCACCACTCAGCTGATTTTGTATTTTAGTAG 17460  
Qy 17717 AGACCGGTTTCGCCACGTTGGCCAGGCTGGTCTGGAATCTCTGACCTCAGGTGATCCAC 17776  
Db 17461 AGACCGGTTTCGCCACGTTGGCCAGGCTGGTCTGGAATCTCTGACCTCAGGTGATCCAC 17520  
Qy 17777 CGGCTTCGGCTCCCAAGTGTGGGATACAGGCTGAGCCACACGCCAGCTGCAAC 17836  
Db 17521 CGGCTTCGGCTCCCAAGTGTGGGATACAGGCTGAGCCACACGCCAGCTGCAAC 17580  
Qy 17837 TTTGATTTCTAGTAGGAAGCCAAATTGCATCTGTGTGAGTGGCTGTGGAAGAGATT 17896  
Db 17581 TTTGATTTCTAGTAGGAAGCCAAATTGCATCTGTGTGAGTGGCTGTGGAAGAGATT 17640  
Qy 17897 TTGGTGTTCGGGATTTGAGCGAATGGTGGGCTTCAGTCTTCAATCTTGAGAGGCGGG 17956  
Db 17641 TTGGTGTTCGGGATTTGAGCGAATGGTGGGCTTCAGTCTTCAATCTTGAGAGGCGGG 17700  
Qy 17957 GCCAGAACAGTGGTCTGATAGTTGGCGGTGGTCTGGCGGTGGAGATTCTCAGGTAGCA 18016  
Db 17701 GCCAGAACAGTGGTCTGATAGTTGGCGGTGGTCTGGCGGTGGAGATTCTCAGGTAGCA 17760  
Qy 18017 GGAATAGCACCTTAGGCGCTCCCGAGGATGGCTAGGTGCTCTGAATTTCTGTTGGG 18076  
Db 17761 GGAATAGCACCTTAGGCGCTCCCGAGGATGGCTAGGTGCTCTGAATTTCTGTTGGG 17820  
Qy 18077 TGCATCTGAAACCTTCCAGCTGTCTCTGAGTGATCAGGAAGAAATTTCTCTACTCTGG 18136  
Db 17821 TGCATCTGAAACCTTCCAGCTGTCTCTGAGTGATCAGGAAGAAATTTCTCTACTCTGG 17880  
Qy 18137 GTAGATGGATCCGCTCTTAAGCCCATGACATTCCTCCGAGGACCGCTGATTTCTGTA 18196  
Db 17881 GTAGATGGATCCGCTCTTAAGCCCATGACATTCCTCCGAGGACCGCTGATTTCTGTA 17940  
Qy 18197 TGGAGTACGTACACCGGGGAGACTTGATGTACCACATTCACAGCTGGGCAAGTTTAAAG 18256  
Db 17941 TGGAGTACGTACACCGGGGAGACTTGATGTACCACATTCACAGCTGGGCAAGTTTAAAG 18000  
Qy 18257 AGCCCATATGAGGCTGAGTCTCGGCCAAACAGAGAATGGTGGGGTGGTGGAGGGGGCAG 18316  
Db 18001 AGCCCATATGAGGCTGAGTCTCGGCCAAACAGAGAATGGTGGGGTGGTGGAGGGGGCAG 18060  
Qy 18317 GATCCAGCCATGACCTTCTGAGTCTCCACCCACCCCGCTCTCAGGTTCTACCGGCA 18376  
Db 18061 GATCCAGCCATGACCTTCTGAGTCTCCACCCACCCCGCTCTCAGGTTCTACCGGCA 18120  
Qy 18377 GAAATCGCTATCGGCTCTTCTTCTTCAATCAGGGCATCATCTACAGGTGAGCAGCC 18436  
Db 18121 GAAATCGCTATCGGCTCTTCTTCTTCAATCAGGGCATCATCTACAGGTGAGCAGCC 18180  
Qy 18437 CAGGAAATTCGTGGAGGAATCAGCCCTCGGAAGGGAAGGATTTGAAATATGTGGCT 18496  
Db 18181 CAGGAAATTCGTGGAGGAATCAGCCCTCGGAAGGGAAGGATTTGAAATATGTGGCT 18240  
Qy 18497 CTAGACTGCTGAATCAACACTTCTTGCAATTCCTGCCACACCCCGCTGCATCGTCCAG 18556  
Db 18241 CTAGACTGCTGAATCAACACTTCTTGCAATTCCTGCCACACCCCGCTGCATCGTCCAG 18300  
Qy 18557 GACCTGAAGCTGACAAATGTGATGTGATGTGAGGGAACATCAAGATCACTGATTTT 18616  
Db 18301 GACCTGAAGCTGACAAATGTGATGTGATGTGAGGGAACATCAAGATCACTGATTTT 18360  
Qy 18617 GGCATGTGAAGAGAACGTTCTCCCGGAGACCAACCGGACCTTCTGCGGACCCCG 18676  
Db 18361 GGCATGTGAAGAGAACGTTCTCCCGGAGACCAACCGGACCTTCTGCGGACCCCG 18420  
Qy 18677 GACTACATAGCCCGGAGGTAAACCCACCTCTGCTCTGTTGTCAGCTTTTGAGATCCCT 18736  
Db 18421 GACTACATAGCCCGGAGGTAAACCCACCTCTGCTCTGTTGTCAGCTTTTGAGATCCCT 18480  
Qy 18737 TAGAGGGTGTAGTGTGATGTTTCAACCGGTTGAGGCTGACCTCAGACCTTG 18796  
Db 18481 TAGAGGGTGTAGTGTGATGTTTCAACCGGTTGAGGCTGACCTCAGACCTTG 18540

Qy 18797 TCATGAGTTGTGGCTTCTTACACAGCCAGTGGTCTCTCCAGCCTCCAGCACAGGTGAGC 18856  
Db 18541 TCATGAGTTGTGGCTTCTTACACAGCCAGTGGTCTCTCCAGCCTCCAGCACAGGTGAGC 18600  
Qy 18857 TTGGCACTGAGCCTGCCAGGTGGGCCAGGCTGCTCTAAATAGGTAAAGTGGGAGCA 18916  
Db 18601 TTGGCACTGAGCCTGCCAGGTGGGCCAGGCTGCTCTAAATAGGTAAAGTGGGAGCA 18660  
Qy 18917 CCTGTGGTGAATGTTTCAGAGAGTGGGACCAGCTCGTAGGAATTCAGTAGGACCTG 18976  
Db 18661 CCTGTGGTGAATGTTTCAGAGAGTGGGACCAGCTCGTAGGAATTCAGTAGGACCTG 18720  
Qy 18977 ACCCTGAGTCTCTGAGAGGGGACAGATTTCTAGTGTACTCTCAGTGGGTGGGCC 19036  
Db 18721 ACCCTGAGTCTCTGAGAGGGGACAGATTTCTAGTGTACTCTCAGTGGGTGGGCC 18780  
Qy 19037 TGTCCCTGCCCCAACACACTCCGAGCTATCTTCTGAATACTTTAACTGGGAGG 19096  
Db 18781 TGTCCCTGCCCCAACACACTCCGAGCTATCTTCTGAATACTTTAACTGGGAGG 18840  
Qy 19097 GCTCTCCTGGAGTATTCAGTTGATGGAAGCTTATTTCTGTTGTTGTAAGTGTCTCT 19156  
Db 18841 GCTCTCCTGGAGTATTCAGTTGATGGAAGCTTATTTCTGTTGTTGTAAGTGTCTCT 18900  
Qy 19157 GATGTAGTGTACTGGACTTCTGTGCTGCATTTTCAAGAGGACAGATCAGCTGGGCGC 19216  
Db 18901 GATGTAGTGTACTGGACTTCTGTGCTGCATTTTCAAGAGGACAGATCAGCTGGGCGC 18960  
Qy 19217 GGTGGCTCACACCTGTAAATCCAGCACTTTGGGAGGTGAGGAGGTGGATCACTTGA 19276  
Db 18961 GGTGGCTCACACCTGTAAATCCAGCACTTTGGGAGGTGAGGAGGTGGATCACTTGA 19020  
Qy 19277 TCAGAGTTTGAAGACAGCCTGGGCCAATGGTGAACCTCATCTCTAAACAAATTAAC 19336  
Db 19021 TCAGAGTTTGAAGACAGCCTGGGCCAATGGTGAACCTCATCTCTAAACAAATTAAC 19080  
Qy 19337 AAATTTAGCCGGCTGGTGGCATCGCTGTAAATCCAGCTTATTTGGGAGGCTGAGG 19396  
Db 19081 AAATTTAGCCGGCTGGTGGCATCGCTGTAAATCCAGCTTATTTGGGAGGCTGAGG 19140  
Qy 19397 GAGAAATCGTTGAAACCGGGAGGCGGAGTTGCAAGTGTGAGTGTGAGATCAACACTG 19456  
Db 19141 GAGAAATCGTTGAAACCGGGAGGCGGAGTTGCAAGTGTGAGTGTGAGATCAACACTG 19200  
Qy 19457 CCAGCTGGGTGACAGAGCATTAATCTCATTAATCTCAAAACAAACAAACAAACAA 19516  
Db 19201 CCAGCTGGGTGACAGAGCATTAATCTCATTAATCTCAAAACAAACAAACAAACAA 19260  
Qy 19517 GCCGGTGCAGTGGCTCACACTGTAAATCCAGCACTTTGGGAGGCTGAGGCGGCGGATC 19576  
Db 19261 GCCGGTGCAGTGGCTCACACTGTAAATCCAGCACTTTGGGAGGCTGAGGCGGCGGATC 19320  
Qy 19577 ACAAGGTGAGAGTTTGAGACCGCTGACATGATGGTGAATCTCACTCTACTATAAA 19636  
Db 19321 ACAAGGTGAGAGTTTGAGACCGCTGACATGATGGTGAATCTCACTCTACTATAAA 19380  
Qy 19637 ATACAAATTTAGCAGCGGTGGGGTGGCTGTAGTCCAGCTACTTTGGGAGGCTG 19696  
Db 19381 ATACAAATTTAGCAGCGGTGGGGTGGCTGTAGTCCAGCTACTTTGGGAGGCTG 19440  
Qy 19697 AGGAGGAGAAATTAATCTTGAACCCCGGAGGTGGAGTTGCACTGAGTGTGAGATTCG 19756  
Db 19441 AGGAGGAGAAATTAATCTTGAACCCCGGAGGTGGAGTTGCACTGAGTGTGAGATTCG 19500  
Qy 19757 TGCATCTCAGTCTGGGCAACAGAGTGAGACCTCTCTCAAAACAAACAAACAAACAA 19816  
Db 19501 TGCATCTCAGTCTGGGCAACAGAGTGAGACCTCTCTCAAAACAAACAAACAAACAA 19560  
Qy 19817 AGAAAGGGCAGGCTGAGATCCCTTAAGTTCTGGGAGGACAGATGCTGTCTATGAGTA 19876  
Db 19561 AGAAAGGGCAGGCTGAGATCCCTTAAGTTCTGGGAGGACAGATGCTGTCTATGAGTA 19620

QY	19877	TTTTAAGTGGGTGGGTATTAACCGACTTTCTTAAGGGGTGGGCTGATGTTCTGAATG	19936		Db	20701	CAGAGGGGCTTAGGCTTCTTAAAGAACGATCATGATTCCTCGCTTCACCTCCCTA	20760
Db	19621	TTTTAAGTGGGTGGGTATTAACCGACTTTCTTAAGGGGTGGGCTGATGTTCTGAATG	19680		QY	21017	GATCATTGCTTACCGCCCTATGCGAAGTCTGTGCAATGGTGGTCTCTTTGGAGTCTTGCT	21076
QY	19937	TACGTATAGATGGATAAAGCACATGCCCTGTAGTCCAGCTACTTTGGGAGGATGTGCCCTGA	19996		Db	20761	GATCATTGCTTACCGCCCTATGCGAAGTCTGTGCAATGGTGGTCTCTTTGGAGTCTTGCT	20820
Db	19681	TACGTATAGATGGATAAAGCACATGCCCTGTAGTCCAGCTACTTTGGGAGGATGTGCCCTGA	19740		QY	21077	GTATGAGATGTTGGCAGGACAGGTAAAGGAAGGTGGGAGAGAGCTGGCTTGGCTTAAAGA	21136
QY	19997	CTCGTGCCCAATTAATCAATGCTAGTGATCAAAACCTGGCTGGTAAATCAGAAATCATCT	20056		Db	20821	GTATGAGATGTTGGCAGGACAGGTAAAGGAAGGTGGGAGAGAGCTGGCTTGGCTTAAAGA	20880
Db	19741	CTCGTGCCCAATTAATCAATGCTAGTGATCAAAACCTGGCTGGTAAATCAGAAATCATCT	19800		QY	21137	GACAGAGGGGCACCTGCTGATCTCAGAGAGAGCCAGTGTAGAAAGGAGCCACAGAGTGTGT	21196
QY	20057	GTAGAAAATTTGAAAATCTGAGGCCAGACATGGTGGCTCATGCCCTGTAAATCCCAGCACTTT	20116		Db	20881	GACAGAGGGGCACCTGCTGATCTCAGAGAGAGCCAGTGTAGAAAGGAGCCACAGAGTGTGT	20940
Db	19801	GTAGAAAATTTGAAAATCTGAGGCCAGACATGGTGGCTCATGCCCTGTAAATCCCAGCACTTT	19860		QY	21197	GCTCGAATACGCTGTCCATGGTCTGAAAGTGTGTCTTAAATGTAGACACAGGTGTTTTGT	21256
QY	20117	GGGAGCTGAGGCGAGGAGATCACTTGAGGTTCAGGAATTCAGAACCCAGCTTACGCCAATCAT	20176		Db	20941	GCTCGAATACGCTGTCCATGGTCTGAAAGTGTGTCTTAAATGTAGACACAGGTGTTTTGT	21000
Db	19861	GGGAGCTGAGGCGAGGAGATCACTTGAGGTTCAGGAATTCAGAACCCAGCTTACGCCAATCAT	19920		QY	21257	TTTGTGTTTTGTTTTGTTTTGTTTACCATGATTCCTTCTCCCTAGATGGTAAAGTAGC	21316
QY	20177	GGTGAACCCCGTCTCTACTAAAAATACAAAATTTAGCTGGACATGGTGTGTGTGCGCTG	20236		Db	21001	TTTGTGTTTTGTTTTGTTTTGTTTACCATGATTCCTTCTCCCTAGATGGTAAAGTAGC	21060
Db	19921	GGTGAACCCCGTCTCTACTAAAAATACAAAATTTAGCTGGACATGGTGTGTGTGCGCTG	19980		QY	21317	AGTCTGGTTTAAGCCCTATGGATCCCTTCTCAGAAAGATGTTTTCAATGCACAAAATAGAA	21376
QY	20237	TCAACCCAGCTACTCAGAGGCTGAGCGAGAGATCACTTGAACCCAGGAGGTGGAGGT	20296		Db	21061	AGTCTGGTTTAAGCCCTATGGATCCCTTCTCAGAAAGATGTTTTCAATGCACAAAATAGAA	21120
Db	19981	TCAACCCAGCTACTCAGAGGCTGAGCGAGAGATCACTTGAACCCAGGAGGTGGAGGT	20040		QY	21377	TAATACATACGAGAAAACCAAGGTTCAAAATCCTCACTTGGCCACTTACTGGCTGTGTCA	21436
QY	20297	TGCAGTGAGCCAGATTTGCCACCACTGCACTGCCATCTCTGGCTACAGAGTGAGACTCCATC	20356		Db	21121	TAATACATACGAGAAAACCAAGGTTCAAAATCCTCACTTGGCCACTTACTGGCTGTGTCA	21180
Db	20041	TGCAGTGAGCCAGATTTGCCACCACTGCACTGCCATCTCTGGCTACAGAGTGAGACTCCATC	20100		QY	21437	GCTTAGACAAATTACATACATCTTAATCAGCTTGAATGGATTCCTGGAGTGCCTGAGTGTA	21496
QY	20357	TCAAAAAGAAAAGATAAGAAAATTTGAAAATACACATATTCCTGACTCTGCAC	20416		Db	21181	GCTTAGACAAATTACATACATCTTAATCAGCTTGAATGGATTCCTGGAGTGCCTGAGTGTA	21240
Db	20101	TCAAAAAGAAAAGATAAGAAAATTTGAAAATACACATATTCCTGACTCTGCAC	20160		QY	21497	CTAACCTTAAAAAATTTGGTTACCACTCTTTGATCATCTTCTTAGCTGGCTATGGTAGT	21556
QY	20417	AAATATTCTAGTGGGTGGAAACCAAGTGTGGCGGTAGGTAGTCTTTCTATTTCAGGC	20476		Db	21241	CTAACCTTAAAAAATTTGGTTACCACTCTTTGATCATCTTCTTAGCTGGCTATGGTAGT	21300
Db	20161	AAATATTCTAGTGGGTGGAAACCAAGTGTGGCGGTAGGTAGTCTTTCTATTTCAGGC	20220		QY	21557	GGGCACTTATAGTCCAGCTACTGGGAGGCTGAGCGAGGAGGTCAATGAGCCCAAGA	21616
QY	20477	CAAAATGAATTTGAAGTAGGTATGCTTTGTTTCCAGAAATTTCCAAAAGTTAGATCGCT	20536		Db	21301	GGGCACTTATAGTCCAGCTACTGGGAGGCTGAGCGAGGAGGTCAATGAGCCCAAGA	21360
Db	20221	CAAAATGAATTTGAAGTAGGTATGCTTTGTTTCCAGAAATTTCCAAAAGTTAGATCGCT	20280		QY	21617	ACTCAAGGTTACACTGAATATGATATGCCACTGTGTTCAGCACAGCGCAGCAGCAA	21676
QY	20537	GGCCAAAATTTACAGAGTGAGGCTGGCGTGTGTGCTCACTCTATATATCCAGCACTT	20596		Db	21361	ACTCAAGGTTACACTGAATATGATATGCCACTGTGTTCAGCACAGCGCAGCAGCAA	21420
Db	20281	GGCCAAAATTTACAGAGTGAGGCTGGCGTGTGTGCTCACTCTATATATCCAGCACTT	20340		QY	21677	GACCCCATCTCAAAAGAAACAAACAAACAAAGAAATCAATCAATTTGAAAGATAGTCACC	21736
QY	20597	TGGGAGCGGAGGAGCCCAATTTGCTTTGAGTCCGGAGTTTGAGACAGCCTGGGCAACA	20656		Db	21421	GACCCCATCTCAAAAGAAACAAACAAACAAAGAAATCAATCAATTTGAAAGATAGTCACC	21480
Db	20341	TGGGAGCGGAGGAGCCCAATTTGCTTTGAGTCCGGAGTTTGAGACAGCCTGGGCAACA	20400		QY	21737	AAAATTTTAAAAATTTAAATGAACTTAAACCAACCAACTAAATGATATACAGTTGTCT	21796
QY	20657	TAGTAGGACCTATCTTCAATAAGTGCAAAATTTAGCCAGGTGTGGTGGCACACCT	20716		Db	21481	AAAATTTTAAAAATTTAAATGAACTTAAACCAACCAACTAAATGATATACAGTTGTCT	21540
Db	20401	TAGTAGGACCTATCTTCAATAAGTGCAAAATTTAGCCAGGTGTGGTGGCACACCT	20460		QY	21797	AAAATTTTAAAAATTTAAATGAACTTAAACCAACCAACTAAATGATATACAGTTGTCT	21856
QY	20717	GTAGCCCACTACTCGGAGGCTGAGGTAGAGAAATTAATCTGAGCCCTGGGAAGTTGAGGC	20776		Db	21541	AAAATTTTAAAAATTTAAATGAACTTAAACCAACCAACTAAATGATATACAGTTGTCT	21600
Db	20461	GTAGCCCACTACTCGGAGGCTGAGGTAGAGAAATTAATCTGAGCCCTGGGAAGTTGAGGC	20520		QY	21857	AGTTCTAATGTTAGTAAAGTAAAGAGGAGCTCTAACAGTAAATTTTGTAGTAGCAATGACT	21916
QY	20777	TGAGTGAGCGGTGATCACTACTGTGCTCCAGCCTGGGCAACAGAGTGAGACCCCTGTCA	20836		Db	21601	AGTTCTAATGTTAGTAAAGTAAAGAGGAGCTCTAACAGTAAATTTTGTAGTAGCAATGACT	21660
Db	20521	TGAGTGAGCGGTGATCACTACTGTGCTCCAGCCTGGGCAACAGAGTGAGACCCCTGTCA	20580		QY	21917	AATAATTTGGGAATATCTGCAACTCTCATGTGATGAGAAAATACCTGTGATTAATGAT	21976
QY	20837	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	20896		Db	21661	AATAATTTGGGAATATCTGCAACTCTCATGTGATGAGAAAATACCTGTGATTAATGAT	21720
Db	20581	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	20640		QY	21977	AATGAGCCCAAGCAGCTGCTGCCCTGCATTAATCTGAGGGAATGCTTAATTTTA	22036
QY	20897	GAGTGGGAAGAGCTTGTGCTGAAGCAGCTTAAGCTGGGTAGCGCTCCAGGGGGTGGGC	20956		Db	21721	AATGAGCCCAAGCAGCTGCTGCCCTGCATTAATCTGAGGGAATGCTTAATTTTA	21780
Db	20641	GAGTGGGAAGAGCTTGTGCTGAAGCAGCTTAAGCTGGGTAGCGCTCCAGGGGGTGGGC	20700		QY	22037	GTTAGAGCTTAAAAAATAAATTTGGCCGGACATGGTGGCTCACGCCCTGTAATCCAGCACT	22096
QY	20957	CAGAGGGGTCTTAGGCTTCTTAAAGAACGATCATGATTCCTGCTTCCACCTCCCTTA	21016					



Db	21781	GTAGAGTTAAATAAATTTTGGCGGACATGTTGGCTCACGCCCTGTAATCCAGCACT	21840
Qy	22097	TTGGAGGCGGAAGTGGGAGATCACTTGAGGTGAGAGTTTGAGACGAGCCTGGCCAAAT	22156
Db	21841	TTGGAGGCGGAAGTGGGAGATCACTTGAGGTGAGAGTTTGAGACGAGCCTGGCCAAAT	21900
Qy	22157	ATGATGAACCCCATCTCTAAATCTTTGCTTGGTATCATTTTGTAACTCAGAAGAC	22216
Db	21901	ATGATGAACCCCATCTCTAAATCTTTGCTTGGTATCATTTTGTAACTCAGAAGAC	21960
Qy	22217	TGTGAATCTACTCATCCAAACAGGAGAAATCTTTTAGGGTGTTCCTGCAAGTTTTCCTCT	22276
Db	21961	TGTGAATCTACTCATCCAAACAGGAGAAATCTTTTAGGGTGTTCCTGCAAGTTTTCCTCT	22020
Qy	22277	CTTCTATTAACTGACATGTTGCATTAATTAACAGCCTGCTGATTTTACATAGCAGATAAAG	22336
Db	22021	CTTCTATTAACTGACATGTTGCATTAATTAACAGCCTGCTGATTTTACATAGCAGATAAAG	22080
Qy	22337	AGAGGCAGAAATAGTACAGAGATGCACAGATCTTGAGGCATCCGAGATAGGAAATGAGAGAA	22396
Db	22081	AGAGGCAGAAATAGTACAGAGATGCACAGATCTTGAGGCATCCGAGATAGGAAATGAGAGAA	22140
Qy	22397	CCTGAGAAAGCAGAGATCAAGCTTTGGTGTGGTCTGATCTCTCTGAGGGTGTGGT	22456
Db	22141	CCTGAGAAAGCAGAGATCAAGCTTTGGTGTGGTCTGATCTCTCTGAGGGTGTGGT	22200
Qy	22457	CAGGTGTGATGTGGGCGTGTGATGGGTGAGGCATGTTCCGGTGGGTGAGGAGGGTG	22516
Db	22201	CAGGTGTGATGTGGGCGTGTGATGGGTGAGGCATGTTCCGGTGGGTGAGGAGGGTG	22260
Qy	22517	TGGAAGTTTGGGAAAGGACGTTGGGCATGTCCTGACTCTCTATCCCTCCACTTTGA	22576
Db	22261	TGGAAGTTTGGGAAAGGACGTTGGGCATGTCCTGACTCTCTATCCCTCCACTTTGA	22320
Qy	22577	TAGCCTCCCTTCGATGGGAGGACGAGGAGAGCTGTTTCAGGCCATCATGAAACAAACT	22636
Db	22321	TAGCCTCCCTTCGATGGGAGGACGAGGAGAGCTGTTTCAGGCCATCATGAAACAAACT	22380
Qy	22637	GTCACCTACCCAGTCGCTTTCCGGGAAGCGGTGGCCATCTGCAAGGGGTGAGGCC	22696
Db	22381	GTCACCTACCCAGTCGCTTTCCGGGAAGCGGTGGCCATCTGCAAGGGGTGAGGCC	22440
Qy	22697	CCCTGACTCCAGCTTCTCAGGCTCACAAACACACACACCCATGCTGCTCTGTCCTA	22756
Db	22441	CCCTGACTCCAGCTTCTCAGGCTCACAAACACACACACCCATGCTGCTCTGTCCTA	22500
Qy	22757	TTAGAAAAATGCTCCCATTCCTGAAGTCACTTTACTTTCATCTGTTGGAAGTTGATAT	22816
Db	22501	TTAGAAAAATGCTCCCATTCCTGAAGTCACTTTACTTCCATCTGTTGGAAGTTGATAT	22560
Qy	22817	GATGCATAGGTTTGTAGAACATGATTTCCAGCCCTGTTGCCACGAGCCCTGGAGATG	22876
Db	22561	GATGCATAGGTTTGTAGAACATGATTTCCAGCCCTGTTGCCACGAGCCCTGGAGATG	22620
Qy	22877	GCCTCTGCTCATCTCTTCTGTGACTCCCACTCCCACTCCCTGCTTGCAGGAAGTGC	22936
Db	22621	GCCTCTGCTCATCTCTTCTGTGACTCCCACTCCCACTCCCTGCTTGCAGGAAGTGC	22680
Qy	22937	TGAAAGTCAGGGTGTCTGTCTGTCTAGAACTGGGTGGGTGAGGTAAACCAACTTCTGC	22996
Db	22681	TGAAAGTCAGGGTGTCTGTCTGTCTAGAACTGGGTGGGTGAGGTAAACCAACTTCTGC	22740
Qy	22997	AGCTTTTCTCTGTGTGAACCTTGGGTGAGTCACCAAAATTTTGTGAGCTTAACTCTCTT	23056
Db	22741	AGCTTTTCTCTGTGTGAACCTTGGGTGAGTCACCAAAATTTTGTGAGCTTAACTCTCTT	22800
Qy	23057	CAGGGGTTATGGAGTTGACACAGAGAAAGCACCTGGGCCCATAGCAGATTTTTCAGCCCAT	23116
Db	22801	CAGGGGTTATGGAGTTGACACAGAGAAAGCACCTGGGCCCATAGCAGATTTTTCAGCCCAT	22860
Qy	23117	GTCAGACCTTCTGGGTCTAGTGTCTCTCTGCACTCCCTGACAGTCTCTCTGGTTTC	23176
Db	22861	GTCAGACCTTCTGGGTCTAGTGTCTCTCTGCACTCCCTGACAGTCTCTCTGGTTTC	22920

Qy	23177	TGCTCATGCTCCCTCCATCTGCATACGATGGGGCTCTCTGTTGTTTCTTCTCTCTC	23236
Db	22921	TGCTCATGCTCCCTCCATCTGCATACGATGGGGCTCTCTGTTGTTTCTTCTCTCTC	22980
Qy	23237	TGCTCTCCCTTCTGCATCTCTGTCTACACATTTTGGGGCTTTGTCCAAACCCCTTACC	23296
Db	22981	TGCTCTCCCTTCTGCATCTCTGTCTACACATTTTGGGGCTTTGTCCAAACCCCTTACC	23040
Qy	23297	CATCTCTGCTCCCTCCTGTGTGCTCATACACACAGCTATCTCAGCCTCTCTC	23356
Db	23041	CATCTCTGCTCCCTCCTGTGTGCTCATACACACAGCTATCTCAGCCTCTCTC	23100
Qy	23357	CTGCTGGCTTCTGTCTCTCCCTTTCTCTGGGTCTCTGTGCCCATATTTGGTCTTTATTC	23416
Db	23101	CTGCTGGCTTCTGTCTCTCCCTTTCTCTGGGTCTCTGTGCCCATATTTGGTCTTTATTC	23160
Qy	23417	CTCCCTCTGGGTGTGTTGTTCTGGGTCTCTATCCTTCTCTCTTCTGAAATCTCTGCC	23476
Db	23161	CTCCCTCTGGGTGTGTTGTTCTGGGTCTCTATCCTTCTCTCTTCTGAAATCTCTGCC	23220
Qy	23477	CCTGGGTCTCTGTCTCTCCCTCTCTCTGAGTTTCTGAGTTTCTTACCTGGGTCTCTG	23536
Db	23221	CCTGGGTCTCTGTCTCTCCCTCTCTCTGAGTTTCTTACCTGGGTCTCTG	23280
Qy	23537	TACCACCTCTGAAATTTCTATTTCCCTTTTCTCTGGGTCTGCAACCTCTCTTCCCCCAT	23596
Db	23281	TACCACCTCTGAAATTTCTATTTCCCTTTTCTCTGGGTCTGCAACCTCTCTTCCCCCAT	23340
Qy	23597	TCCCTCCCTCTTCCCTCTCTCTACCTCTACCTCTCTCTCTCTCTCTCTCTCTCTCT	23656
Db	23341	TCCCTCCCTCTTCCCTCTCTCTACCTCTACCTCTCTCTCTCTCTCTCTCTCTCTCT	23400
Qy	23657	CTGTCTCTCACTCTCCCT	23716
Db	23401	CTGTCTCTCACTCTCCCT	23460
Qy	23717	CCCTTCCCT	23776
Db	23461	CCCTTCCCT	23520
Qy	23777	TGTTCTGTCTCTGTGTGCTCTGGGTCTCTGGGTATGAAATTTCACTGCTATCATTTT	23836
Db	23521	TGTTCTGTCTCTGTGTGCTCTGGGTCTCTGGGTATGAAATTTCACTGCTATCATTTT	23580
Qy	23837	CATGTAATCT	23896
Db	23581	CATGTAATCT	23640
Qy	23897	GTCT	23956
Db	23641	GTCT	23700
Qy	23957	TCTGTGTGTCT	24016
Db	23701	TCTGTGTGTCT	23760
Qy	24017	CCT	24076
Db	23761	CCT	23820
Qy	24077	CT	24136
Db	23821	CT	23880
Qy	24137	TCTCGGATCTCATGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	24196
Db	23881	TCTCGGATCTCATGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	23940
Qy	24197	CTCTGGGTCTACCTGTCTCGGCACTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT	24256
Db	23941	CTCTGGGTCTACCTGTCTCGGCACTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT	24000







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